

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:16:10 ; Search time 1464 Seconds
(without alignments)
2664.531 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080

Perfect score: 90

Sequence: 1 gaacggatgctgctgca.....gaacgtggaacgactag 90

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	90	100.0	771	6	AX053659	AX053659 Sequence
2	90	100.0	1055	6	AR099307	AR099307 Sequence
3	90	100.0	1659	6	AX024046	AX024046 Sequence
4	90	100.0	2268	6	AR067807	AR067807 Sequence
5	90	100.0	2268	6	AR084022	AR084022 Sequence
6	90	100.0	2268	6	AR153351	AR153351 Sequence
7	90	100.0	2268	6	AR153423	AR153423 Sequence
8	90	100.0	2268	6	AR153426	AR153426 Sequence
9	90	100.0	2268	6	AR253906	AR253906 Sequence
10	90	100.0	2268	6	AR253906	AR253906 Sequence
11	90	100.0	2268	6	AX118491	AX118491 Sequence
12	90	100.0	2268	6	BD062396	BD062396 IKK-alpha
13	90	100.0	2268	6	BD062399	BD062399 IKK-beta
14	90	100.0	2268	9	AF029684	AF029684 Homo sapi
15	90	100.0	2271	6	AR162236	AR162236 Sequence
16	90	100.0	2271	6	AR342527	AR342527 Sequence
17	90	100.0	2271	6	BD009912	BD009912 Stimulus-
18	90	100.0	2271	9	AF031416	AF031416 Homo sapi
19	90	100.0	2783	9	AK091297	AK091297 Homo sapi
20	90	100.0	2818	6	AX880268	AX880268 Sequence
21	90	100.0	2818	6	BD158288	BD158288 Primer fo
22	90	100.0	2931	9	AK023193	AK023193 Homo sapi
23	90	100.0	2931	6	AR156758	AR156758 Sequence
24	90	100.0	3018	6	BD082222	BD082222 I-kappa-B
25	90	100.0	3024	6	AX024044	AX024044 Sequence
26	90	100.0	3058	9	AF080158	AF080158 Homo sapi
27	90	100.0	3785	9	HSM808312	HSM808312 Homo sapi
28	90	100.0	3966	6	AR099305	AR099305 Sequence
29	86	95.6	2404	9	AK097828	AK097828 Homo sapi
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31	86	95.6	186433	2	AF271407	AF271407 Homo sapi
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33	77.2	85.8	3038	10	AF115282	AF115282 Rattus no
34	74	82.2	2274	10	AF026524	AF026524 Mus muscu
35	74	82.2	3572	10	BC037723	BC037723 Mus muscu
36	74	82.2	4039	10	AF088910	AF088910 Mus muscu
37	73.2	81.3	274786	2	AC109661	AC109661 Rattus no
38	70	77.8	225065	10	AC121835	AC121835 Mus muscu
39	68.2	75.8	3490	4	BTM414556	BTM414556 Bos tauru
40	36.2	40.2	3442	4	BTM414555	BTM414555 Bos tauru
41	35.6	39.6	1874	6	AR258658	AR258658 Sequence
42	35.6	39.6	2025	6	AR102061	AR102061 Sequence
43	35.6	39.6	2056	10	BC018243	BC018243 Mus muscu
44	35.6	39.6	3314	6	AR258657	AR258657 Sequence
45	35.6	39.6	3466	6	AX306151	AX306151 Sequence

ALIGNMENTS

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LOCUS	AX053659					
DEFINITION	AX053659					
ACCESSION	AX053659					
VERSION	AX053659.1	GI:12227978				
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE						
AUTHORS	Obata, Y.					
TITLE	Breast, gastric and prostate cancer associated antigens and uses therefor					

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us-09-806-701-15_copy_991_1080.rge

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JOURNAL Patent: WO 0073801-A 425 07-DEC-2000;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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QY 61 AAGCAGGGGGGAACGCTGACGACCTAGAG 90
Db 172 AAGCAGGGGGGAACGCTGACGACCTAGAG 201

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LOCUS
DEFINITION Sequence 3 from patent US 6077701.
ACCESSION AR099307
VERSION AR099307.1 GI:12809073
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1055)
AUTHORS Chu, K. and Pot, D.
TITLE Ikk beta. regulates transcription factors
JOURNAL Patent: US 6077701-A 3 20-JUN-2000;
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Db 322 GAACGGATGATGGCTCTGCAGACCGACATTTGGACTTACAGAGAGCCCATGGGCCGG 381
QY 61 AAGCAGGGGGGAACGCTGACGACCTAGAG 90
Db 382 AAGCAGGGGGGAACGCTGACGACCTAGAG 411

RESULT 3
AX024046 AX024046 1659 bp DNA linear PAT 15-SEP-2000
LOCUS
DEFINITION Sequence 15 from Patent WO0023091.
ACCESSION AX024046
VERSION AX024046.1 GI:10184361
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Scudder, K.M., Thastrup, O., Bjoern, S.P., Terry, B.R. and
Arkhammar, P.O.
TITLE Specific therapeutic interventions obtained by interference with
redistribution and/or targeting
JOURNAL Patent: WO 0023091-A 15 27-APR-2000;
SCUDDER KURT MARSHALL (DK) ; BIOIMAGE A S (DK) ; THASTRUP OLE (DK)
; BJOERN SARA PETERSEN (DK) ; TERRY BERNARD ROBERT (DK) ; ARKHAMMAR
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    MVLEFVTAAGITIGMDELYKSGLSRRAQASTMNLRLNNSCLSKMKNVSLVERMM
    AKLDFFTSIQIDLEKYSQTEFGITSDTKLLLAWEQAVALGRENVEKLIVRRM
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QY 61 AAGCAGGGGGGAACGCTGACGACCTAGAG 90
Db 1051 AAGCAGGGGGGAACGCTGACGACCTAGAG 1080

RESULT 4
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LOCUS
DEFINITION Sequence 1 from patent US 5851812.
ACCESSION AR067807
VERSION AR067807.1 GI:5999029
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2268)
AUTHORS Goeddel, D.V. and Woronicz, J.
TITLE IKK-beta. proteins, nucleic acids and methods
JOURNAL Patent: US 5851812-A 1 22-DEC-1998;
FEATURES
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  Best Local Similarity 100.0%; Pred. No. 1.2e-14;
  Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTTGGACTTACAGAGAGCCCATGGGCCGG 1662
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Db 1663 AAGCAGGGGGGAACGCTGACGACCTAGAG 1692

RESULT 5
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ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2268)
TITLE	Rothe,M., Cao,Z. and Regnier,C.
JOURNAL	IKK- alpha. proteins, nucleic acids and methods
FEATURES	Patent: US 6235512-A 1 22-MAY-2001; Location/Qualifiers 1..2268 /organism="unknown" /mol_type="unassigned DNA"
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Best Local Similarity	100.0%; Pred. No. 1.2e-14;
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LOCUS	AR153426
DEFINITION	Sequence 1 from patent US 6235513.
ACCESSION	AR153426
VERSION	AR153426.1 GI:15120958
KEYWORDS	Location/Qualifiers
SOURCE	1..2268 /organism="unknown" /mol_type="unassigned DNA"
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2268)
TITLE	Rothe,M., Cao,Z. and Regnier,C.
JOURNAL	IKK- alpha. proteins, nucleic acids and methods
FEATURES	Patent: US 6235513-A 1 22-MAY-2001; Location/Qualifiers 1..2268 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match	100.0%; Score 90; DB 6; Length 2268;
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LOCUS	AR253906
DEFINITION	Sequence 1 from patent US 6479266.
ACCESSION	AR253906
VERSION	AR253906.1 GI:27302384
KEYWORDS	Location/Qualifiers
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2268)
TITLE	Rothe,M., Cao,Z. and Regnier,C.
JOURNAL	IKK- alpha. proteins nucleic acids and methods
FEATURES	Patent: US 6479266-A 1 12-NOV-2002; Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 1.2e-14;
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Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 10
AX318491 2268 bp DNA linear PAT 14-DEC-2001
LOCUS
DEFINITION
Sequence 1 from Patent WO0183554.
ACCESSION AX318491
VERSION AX318491.1 GI:17900949
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS May, M. J., Ghosh, S., Findeis, M. A. and Phillips, K.
TITLE Anti-inflammatory compounds and uses thereof
JOURNAL Patent: WO 0183554-A 1 08-NOV-2001;
PRAECLIS Pharmaceuticals Incorporated (US) ; YALE UNIVERSITY (US)
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Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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RESULT 11
BD062396 2268 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION
IKK-alpha proteins, nucleic acids and methods.
ACCESSION BD062396
VERSION BD062396.1 GI:22607999
KEYWORDS JP 2001510346-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2268)
AUTHORS Rothe, M., Cao, Z. and Regnier, C.
TITLE IKK-alpha proteins, nucleic acids and methods
JOURNAL Patent: JP 2001510346-A 1 31-JUL-2001;
TULARIK INC
PN JP 2001510346-A/1
PD 31-JUL-2001
PF 01-JUL-1998 JP 1999507372

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RESULT 13
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MIKE ROTHE, ZHAODAN CAO, CATHERINE REGNIER
PC C12N9/12, C12Q1/48
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CC Topology: Linear;
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RESULT 12
BD062399 2268 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION
IKK-beta proteins, nucleic acids and methods.
ACCESSION BD062399
VERSION BD062399.1 GI:22608002
KEYWORDS JP 2001510347-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2268)
AUTHORS Goeddel, D. V. and Woronicz, J.
TITLE IKK-beta proteins, nucleic acids and methods
JOURNAL Patent: JP 2001510347-A 1 31-JUL-2001;
TULARIK INC
PN JP 2001510347-A/1
PD 31-JUL-2001
PF 01-JUL-1998 JP 1999507373
PR 01-JUL-1997 US 08/887114, 10-JUL-1997 US 08/890853 PI
DAVID V GOEDEL, JOHN WORONICZ
PC C12N9/12, C12Q1/48
CC Strandedness: Double;
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RESULT 13
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LOCUS AF029684 2268 bp mRNA linear PRI 15-NOV-1997
DEFINITION Homo sapiens Ikb kinase-beta (IKK-beta) mRNA, partial cds.
ACCESSION AF029684
VERSION AF029684.1 GI:2599557
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 2268)
MEDLINE Woronicz,J.D., Gao,X., Cao,Z., Rothe,M. and Goeddel,D.V.
PUBMED IkappaB kinase-beta: NF-kappaB activation and complex formation
278 (5339), 865-869 (1997)
AUTHORS Science
TITLE 9800814
PUBMED 9346485
REFERENCE 2 (bases 1 to 2268)
AUTHORS Woronicz,J.D., Gao,X., Cao,Z., Rothe,M. and Goeddel,D.V.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1997) Biology, Tularek, Inc., Two Corporate
Drive, S. San Francisco, CA 94080, USA
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Best Local Similarity 100.0%; Pred. No. 1.2e-14;
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QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
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QY 61 AACGAGGGGGGAAACGCTGGACGACCTAGAG 90
Db 1663 AACGAGGGGGGAAACGCTGGACGACCTAGAG 1692
RESULT 14
LOCUS AR162236 2271 bp DNA linear PAT 17-OCT-2001
DEFINITION AR162236
ACCESSION AR162236
VERSION AR162236.1 GI:16229366
KEYWORDS
SOURCE Unknown.
REFERENCE 8 from patent US 6258579.
AUTHORS Mercurio,F., Zhu,H., Barbosa,M., Li,J.W. and Murray,B.W.
TITLE Stimulus-inducible protein kinase complex and methods of use
therefor
JOURNAL Patent: US 6258579-A 8 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..2271
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 90; DB 6; Length 2271;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
Db 1603 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 1662
QY 61 AACGAGGGGGGAAACGCTGGACGACCTAGAG 90
Db 1663 AACGAGGGGGGAAACGCTGGACGACCTAGAG 1692
Search completed: September 23, 2004, 20:20:32
Job time : 1467 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 08:42:00 ; Search time 330 Seconds
(without alignments)
1158.599 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080

Perfect score: 90

Sequence: 1 gaacggatggtgctctgca.....gaacgctgacacacacag 90

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	506	8	ACH37132 Human end
2	90	100.0	771	4	Aaf22846 Human pro
3	90	100.0	1055	2	Aax89677 C-termina
4	90	100.0	1558	4	Aah33389 Human col
5	90	100.0	1659	3	Aa14961 DNA encod
6	90	100.0	2268	2	Aax08919 Human I k
7	90	100.0	2268	2	Aaz31590 Human inh
8	90	100.0	2268	2	Aav84689 Human IKK
9	90	100.0	2268	2	Aax98271 cDNA enco
10	90	100.0	2268	2	Aax79304 Human IKK
11	90	100.0	2268	3	Aac81425 Human I-k
12	90	100.0	2268	6	Ab96316 Human IKK
13	90	100.0	2268	7	Abx11974 Human IKK
14	90	100.0	2268	8	AcD66625 Human inh
15	90	100.0	2271	2	Aax22842 DNA encod
16	90	100.0	2818	4	Aah16296 Human cDN
17	90	100.0	2931	2	Aav32970 Human I-k
18	90	100.0	2998	3	Aaf21148 Human low
19	90	100.0	3018	3	Aa14960 DNA encod
20	90	100.0	3024	3	Aa14958 DNA encod
21	90	100.0	3058	3	Aa14958 DNA encod
22	90	100.0	3058	3	Aa35026 Human ade
23	90	100.0	3965	2	Abz96842 Human nuc
					Aax89675 Full leng

24	90	100.0	8631	3	AAA35028	Human ade
25	90	100.0	8631	3	Aaf21150	Human low
26	90	100.0	8631	7	ABZ96844	Human nuc
27	81.6	90.7	400	7	ACD92547	Human col
28	77.2	85.8	3038	8	ACD66707	Rat inhib
29	74	82.2	554	9	ADD34950	Mouse inh
30	74	82.2	2274	8	ACD66672	Mouse inh
31	35.6	39.6	1874	7	ABX94013	Mouse I k
32	35.6	39.6	1875	8	ADA26740	Mouse I k
33	35.6	39.6	2025	3	AAA08830	cdNA IKK
34	35.6	39.6	3314	7	ABX94012	Murine I
35	35.6	39.6	3314	8	ADA26739	Mouse I k
36	35.6	39.6	3466	6	ABT99798	cdNA IKK
37	35.6	39.6	3466	7	ACC58547	Mouse I k
38	34.6	38.4	2146	2	AAx08917	Mouse IKK
39	34.6	38.4	2146	3	AAc81422	Human ser
40	34.6	38.4	2146	7	ABX11976	Conserved
41	34.6	38.4	2238	2	AAx08918	Human IKK
42	34.6	38.4	2238	2	AAV84690	Human IKK
43	34.6	38.4	2238	2	AAx98272	cdNA enco
44	34.6	38.4	2238	2	AAx79305	Human IKK
45	34.6	38.4	2238	3	AAc81424	Human I-k

ALIGNMENTS

RESULT 1
ACH37132
ID ACH37132 standard; cDNA; 506 BP.
XX
AC ACH37132;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human endothelial cell cDNA #5265.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
FN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 24344; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for

CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antibodies specific for it. The present sequence
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 506 BP; 144 A; 96 C; 167 G; 95 T; 0 U; 4 Other;

Query Match 100.0%; Score 90; DB 8; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGGCTCTGCAGACGACATTTGTGGACTTACAGAGAGCCCATGGGCGG 60
DB 64 GAACGGATGATGGCTCTGCAGACGACATTTGTGGACTTACAGAGAGCCCATGGGCGG 123

QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
DB 124 AAGCAGGGGGGAACGCTGGACGACCTAGAG 153

RESULT 2
AAF22846
ID AAF22846 standard; cDNA; 771 BP.
XX
AC AAF22846;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human prostate cancer associated antigen nucleotide sequence SEQ ID:425.
XX
KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW cancer associated antigen; cytostatic; cancer vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200073801-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014749.
XX
PR 28-MAY-1999; 99US-0136526P.
PR 10-SEP-1999; 99US-0153454P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Obata Y;
XX
DR WPI; 2001-025274/03.
XX
PT Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer.
XX
PS Claim 50; Page 413; 799pp; English.
XX
CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63487, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC

CC e.g. cancer
XX
SQ Sequence 771 BP; 213 A; 176 C; 210 G; 157 T; 0 U; 15 Other;

Query Match 100.0%; Score 90; DB 4; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGGCTCTGCAGACGACATTTGTGGACTTACAGAGAGCCCATGGGCGG 60
DB 112 GAACGGATGATGGCTCTGCAGACGACATTTGTGGACTTACAGAGAGCCCATGGGCGG 171

QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
DB 172 AAGCAGGGGGGAACGCTGGACGACCTAGAG 201

RESULT 3
AA89677
ID AA89677 standard; DNA; 1055 BP.
XX
AC AA89677;
XX
DT 28-SEP-1999 (first entry)
XX
DE C-terminal HLH domain of IKKbeta.
XX
KW inflammatory disease; kinase; NFKappaB; transcription factor; IKKbeta;
KW IKKb; phosphorylation; drug development; C-terminal; ss.
XX
OS Homo sapiens.
XX
PN WO9934000-A1.
XX
PD 08-JUL-1999.
XX
PF 30-DEC-1998; 98WO-US027917.
XX
PR 30-DEC-1997; 97US-0068954P.
PR 18-DEC-1998; 98US-00215131.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chu K, Pot D;
XX
DR WPI; 1999-430247/36.
XX
PT New I-kappa-B kinase polynucleotides and polypeptides.
XX
PS Claim 1; Page 40; 40pp; English.
XX
CC Sequence AA89675 represents the full length DNA sequence of IKKbeta,
CC while sequence AA89676 and AA89677, encode for the N-terminal kinase
CC domain and C-terminal HLH domain of IKKbeta respectively. The proteins
CC may be alternatively spliced forms of IKKbeta. The IKK beta enzyme binds
CC to and phosphorylates I-kappa-B protein. The IKKbeta polypeptides and
CC fragments can be used to raise antibodies, which can then be used in
CC immunochemical assays, to detect the presence of mutations in the
CC IKKappa gene which result in altered expression of the protein, to
CC detect wild type IKKappa in tissue samples. IKKappa polynucleotides are
CC a source of probes and primers, and can be used to produce recombinant
CC protein. The polynucleotides are also a source of antisense sequences,
CC which can be used to decrease expression of the IKKappa gene. The
CC protein can be used to screen for test compounds for use as inflammation
CC inhibitors (claimed). IKK proteins are critical targets for anti-
CC inflammatory drug development
XX
SQ Sequence 1055 BP; 300 A; 248 C; 300 G; 207 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 2; Length 1055;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGGCTCTGACAGCCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
 |||||
 Db 322 GAACGGATGATGGCTCTGACAGCCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 381
 |||||

QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
 |||||
 Db 382 AAGCAGGGGGGAACGCTGGACGACCTAGAG 411
 |||||

RESULT 4
 AAH33389
 ID AAH33389 standard; cDNA; 1558 BP.
 XX
 AC AAH33389;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:445.
 XX
 DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 8; ss.
 KW
 KW Homo sapiens.
 OS
 XX WO2001229220-A2.
 FN
 XX 05-APR-2001.
 PD
 XX
 XX 28-SEP-2000; 2000WO-US026524.
 PF
 XX
 XX 29-SEP-1999; 99US-0157137P.
 PR
 XX 03-NOV-1999; 99US-0163280P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI WPI; 2001-235357/24.
 DR
 XX P-PSDB; AAG73958.
 DR
 XX
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers.
 PT
 XX Claim 1; Page 2542; 9803pp; English.
 XX
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
 CC proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patients own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922
 XX
 XX Query Sequence 1558 BP; 445 A; 372 C; 427 G; 302 T; 0 U; 12 Other;
 SQ
 Query Match 100.0%; Score 90; DB 4; Length 1558;
 Best Local Similarity 100.0%; Pred. No. 1.5e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGGCTCTGACAGCCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
 |||||
 Db 817 GAACGGATGATGGCTCTGACAGCCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 876
 |||||

QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
 |||||
 Db 877 AAGCAGGGGGGAACGCTGGACGACCTAGAG 906
 |||||

RESULT 5
 AAA14961
 ID AAA14961 standard; DNA; 1659 BP.
 XX
 AC AAA14961;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE DNA encoding a GFP-I-kappaB kinase-LZ domain fusion protein.
 XX
 DE I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
 KW cyclic GMP; PDE3; PDE7; PDE8; PDE4 splice variant; PDE4D;
 KW inflammatory disease; chronic inflammation; airway disease; asthma;
 KW chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis;
 KW pelvospodylitis; bowel disease; ulcerative colitis; Crohn's disease;
 KW autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis;
 KW systemic lupus erythematosus; myasthenia gravis; Grave's disease;
 KW immune thrombocytopenic purpura; acute respiratory distress syndrome;
 KW septic shock; depression; PDE1; PDE2; PDE6; PDE9; PDE10; jet lag;
 KW PDE5 splice variant; tension; erectile dysfunction; circadian rhythm;
 KW green fluorescent protein; GFP; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Aequorea victoria.
 XX
 FH Key Location/Qualifiers
 CDS 1..1659
 FT /*tag= a
 FT
 FN WO200023091-A2.
 XX
 XX 27-APR-2000.
 PD
 XX
 XX 15-OCT-1999; 99WO-DK000567.
 PF
 XX 15-OCT-1998; 98DK-00001321.
 PR
 XX 15-OCT-1998; 98DK-00001322.
 PR
 XX 15-OCT-1998; 98DK-00001323.
 PR
 XX (BIOI-) BIOIMAGE AS.
 PA
 XX Arkhammar POG, Terry BR, Scudder KM, Bjorn SP, Thastrup O;
 XX WPI; 2000-399281/34.
 DR P-PSDB; AAY84883.
 DR
 XX Modulating the activity of I-kappaB kinases or cyclic nucleotide
 PT phosphodiesterases for the treatment of inflammatory disorders.
 PT autoimmune disorders (e.g. diabetes and Crohn's disease) and depression.
 XX
 XX Example 3; Page 125-127; 128pp; English.
 PS
 XX The specification describes a method for modulating the specific
 CC effectiveness of I-kappaB kinases or cyclic nucleotide phosphodiesterases
 CC which have the ability to cleave cyclic AMP and/or GMP. This involves
 CC modulating the specific effectiveness of the cyclic nucleotide
 CC phosphodiesterase or I-kappaB kinase by modulating the spatial
 CC distribution within cells of the animal. If the cyclic nucleotide
 CC phosphodiesterase used is a PDE3, PDE7, PDE8 or a splice variant of PDE4
 CC (such as PDE4D), the method is used to treat inflammatory diseases such
 CC as chronic inflammation (especially airway diseases such as asthma and
 CC disorders such as rheumatoid arthritis and pelvospodylitis and bowel
 CC diseases such as ulcerative colitis and Crohn's disease), autoimmune
 CC diseases associated with inflammation (such as diabetes mellitus type I,
 CC systemic lupus erythematosus, myasthenia gravis, Hashimoto's

CC thyroiditis, Grave's disease and immune thrombocytopenic purpura),
CC dysregulations of the immune system (such as acute respiratory distress
CC syndrome (ARDS) and septic shock) and/or depression. Alternatively, if
CC the cyclic nucleotide phosphodiesterase is PDE1, PDE2, PDE6, PDE9, PDE10
CC or a splice variant of PDE5, the method is used to treat hypo- or
CC hypertension, erectile dysfunction, circadian rhythm resetting or jet-
CC lag. The present sequence encodes a fusion protein of green fluorescent
CC protein (GFP) and I-kappaB kinase and the LZ domain, which is used in the
CC course of the invention

XX Sequence 1659 BP; 437 A; 461 C; 486 G; 275 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 3; Length 1659;

Best Local Similarity 100.0%; Pred. No. 1.6e-19; Indels 0; Gaps 0;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGCTCTGCAGACCGACATTTGGACTTACAGAGAGCCCATGGCCCGG 60

DB 991 GAACGGATGATGCTCTGCAGACCGACATTTGGACTTACAGAGAGCCCATGGCCCGG 1050

QY 61 AAGCAGGGGGAAACGCTGGACGACCTAGAG 90

DB 1051 AAGCAGGGGGAAACGCTGGACGACCTAGAG 1080

RESULT 6

AAZ08919

ID AAZ08919 standard; cDNA; 2268 BP.

XX AC

XX AAX08919;

XX 27-APR-1999 (first entry)

XX Human I kappa B kinase coding sequence.

XX I-kappa-B kinase; IKK-alpha; gene expression; modulation; suppression;

KW activation; tumour necrosis factor; TNF; interleukin-1; IL-1;

KW TNF receptor associated factor; TRAF; ds.

XX OS

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..2268

FT /tag= a

FT /label= I_kappa_B_kinase

XX WO9901541-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US013782.

XX 01-JUL-1997; 97US-00887115.

XX 10-JUL-1997; 97US-00890854.

XX (TULA-) TULARIK INC.

XX Rothe M, Cao Z, Regnier C;

XX WPI; 1999-106044/09.

XX P-PSDB; AAW96158.

XX Newly isolated human kinase IkappaB Kinase (IKK- α) polypeptides - useful

PT in screening for agents that modulate the interaction of an IKK

PT polypeptide to a binding target and for modulating signal transduction

PT involving IkappaB in a cell.

XX Disclosure; Page 20; 32pp; English.

XX I-kappa-B, deletion mutants of it retaining I-kappa-B kinase activity and

CC I-kappa-B polypeptides (comprising a six residue domain of I-kappa-B

CC containing one of Ser32 and Ser36, and a candidate agent) can be used to

CC screen for agents that modulate the interaction of an IKK polypeptide to

CC a binding target. The modulation of the kinase activity of IKK-alpha
CC (AAW96157) forms a method for modulating signal transduction involving I-
CC kappa-B in a cell. The IKK-alpha polypeptides are useful for generating
CC oligonucleotide primers and probes for use in the isolation of natural
CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
CC translatable transcripts, hybridization probes, polymerase chain reaction
CC (PCR) probes and primers. Their diagnostic applications include IKK-alpha
CC hybridization probes for identifying wild-type and mutant IKK-alpha
CC alleles in clinical and laboratory samples. Therapeutic application
CC includes the use of IKK-alpha nucleic acids for modulating cellular
CC expression or intracellular concentration/availability of active IKK-
CC alpha. Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
CC activation induced by tissue necrosis factor (TNF), interleukin-1 (IL-1)
CC stimulation, TNF receptor-associated factor (TRAF) and NF-kappa-B-
CC inducing kinase (NIK) overexpression

XX Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 2; Length 2268;

Best Local Similarity 100.0%; Pred. No. 1.7e-19;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGCTCTGCAGACCGACATTTGGACTTACAGAGAGCCCATGGCCCGG 60

DB 1603 GAACGGATGATGCTCTGCAGACCGACATTTGGACTTACAGAGAGCCCATGGCCCGG 1662

QY 61 AAGCAGGGGGAAACGCTGGACGACCTAGAG 90

DB 1663 AAGCAGGGGGAAACGCTGGACGACCTAGAG 1692

RESULT 7

AAZ31590

ID AAZ31590 standard; DNA; 2268 BP.

XX AC

XX AAZ31590;

XX 13-JAN-2000 (first entry)

XX Human inhibitor-kappa B kinase-beta coding sequence.

XX Inhibitor-kappa B kinase-beta; IKB-beta; human; T-cell leukaemia; asthma;

KW inflammatory response; inflammatory disease; juvenile diabetes mellitus;

KW Graves' disease; rheumatoid arthritis; allograft rejection; diagnosis;

KW inflammatory bowel disease; multiple sclerosis; contact dermatitis;

KW rhinitis; allergy; hyperproliferative disorder; tumour; therapy; ss.

XX OS

XX Homo sapiens.

XX US5977341-A.

XX 02-NOV-1999.

XX 20-NOV-1998; 98US-00197008.

XX 20-NOV-1998; 98US-00197008.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Cowser LM;

XX WPI; 1999-619715/53.

XX P-PSDB; AAW43247.

XX Antisense oligonucleotides inhibiting human Inhibitor-kappa B Kinase-

PT beta, useful for treating conditions such as inflammation, asthma,

PT diabetes, allograft rejection, allergies, hyperproliferative disorders or

PT tumors.

XX Claim 1; Col 41-48; 32pp; English.

XX This sequence encodes the human inhibitor-kappa B kinase-beta. The

CC invention relates to an antisense oligonucleotide (I) 8 to 30 nucleotides

CC in length inhibiting the expression of human Inhibitor-kappa B kinase-
 CC beta (IKK-beta). (I) inhibits the expression of human IKK-beta which
 CC plays a role in the development of T-cell leukaemia and in the activation
 CC of inflammatory responses. (I) is therefore useful for treating
 CC inflammatory diseases or disorders with an inflammatory component such as
 CC asthma, juvenile diabetes mellitus, Graves' disease, rheumatoid
 CC arthritis, allograft rejection, inflammatory bowel disease, multiple
 CC sclerosis, contact dermatitis, rhinitis and various allergies, or
 CC hyperproliferative disorders such as leukaemias and other tumours. (I)
 CC may also be used for detection of the above disorders.

XX
 SQ Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 2; Length 2268;
 Best Local Similarity 100.0%; Pred. No. 1.7e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCCGG 60
 Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCCGG 1662
 QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
 Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 8
 AAV84689
 ID AAV84689 standard; cDNA; 2268 BP.
 AC AAV84689;
 XX
 DT 03-MAR-1999 (first entry)
 DE Human IKK-beta polypeptide encoding cDNA.
 KW IKK-beta; IkappaB kinase; inhibitor; NF-kappaB; nuclear factor-kappaB;
 KW nuclear translocation; NF-kappaB-inducing kinase; NIK; recombinant;
 KW human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2268
 FT /*tag= a
 FT /product= "IKK-beta polypeptide"
 FT /note= "the stop codon is not indicated"

US5851812-A.
 XX
 PD 22-DEC-1998.
 XX
 PF 10-JUL-1997; 97US-00890853.
 XX
 PR 01-JUL-1997; 97US-00887114.
 XX
 PA (TULA-) TULARIK INC.
 PI Woronicz J, Goeddel DV;
 XX
 CC WPI; 1999-080407/07.
 DR P-PSDB; AAW86163.
 XX
 FT DNA encoding IKK-beta polypeptides - useful for producing recombinant
 FT polypeptides.
 XX
 PS Claim 3; Col 11-14; 13pp; English.
 XX
 CC This cDNA encodes a IKK-beta (IkappaB kinase) polypeptide. The IkappaB
 CC (inhibitor of nuclear factor (NF)-kappaB nuclear translocation) kinase is
 CC a NF-kappaB-inducing kinase (NIK)-interacting protein. A host cell
 CC containing a recombinant nucleic acid encoding the IKK-beta polypeptide
 CC can be used for the recombinant production of the polypeptide

XX
 SQ Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 2; Length 2268;
 Best Local Similarity 100.0%; Pred. No. 1.7e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCCGG 60
 Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCCGG 1662
 QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
 Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 9
 AAX98271
 ID AAX98271 standard; cDNA; 2268 BP.
 XX
 AC AAX98271;
 XX
 DT 20-MAR-2003 (revised)
 DT 01-OCT-1999 (first entry)
 XX
 DE cDNA encoding human kinase I-kappa-B kinase (IKK-beta).
 XX
 KW Nuclear factor kappa-B inducing kinase; NIK; NIK-interacting protein;
 KW human; I-kappa-B kinase; IKK-beta; IKK-beta disorder; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2268
 FT /*tag= a
 FT /note= "no termination codon given"
 XX
 PN US5939302-A.
 XX
 PD 17-AUG-1999.
 XX
 PF 17-JUN-1998; 98US-00099124.
 XX
 PR 01-JUL-1997; 97US-00887114.
 PR 10-JUL-1997; 97US-00890853.
 XX
 PA (TULA-) TULARIK INC.
 PI Woronicz J, Goeddel DV;
 XX
 CC WPI; 1999-468406/39.
 DR P-PSDB; AAY24051.
 XX
 FT Polypeptides comprising a novel I-kappa-B Kinase useful as hybridization
 FT probes.
 XX
 PS Claim 4; Col 11-14; 13pp; English.

XX
 CC The present sequence encodes a human I-kappa-B kinase (IKK-beta). The
 CC protein is a nuclear factor kappa-B inducing kinase (NIK) interacting
 CC protein. The IKK-beta nucleic acids, polypeptides, and/or antibodies may
 CC be useful as hybridization primers or probes, translatable transcripts,
 CC diagnostic probes (e.g. for identifying the presence of IKK-beta in a
 CC sample), to detect mutant IKK-beta alleles, in the diagnosis and therapy
 CC of IKK-beta disorders, and in the identification of compounds or agents
 CC that are able to modulate IKK-beta function. (Updated on 20-MAR-2003 to
 CC correct PF field.)
 XX
 SQ Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 2; Length 2268;
 Best Local Similarity 100.0%; Pred. No. 1.7e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAACCGATCATCGCTCTGCAGACCGACACATTGTGGACTTTACAGAGGAGCCCCCATGGCGCGG	60
Db	1603	GAACCGATCATCGCTCTGCAGACCGACACATTGTGGACTTTACAGAGGAGCCCCCATGGCGCGG	1662
QY	61	AAGCAGGGGGGAACGCTGGACGACCTTAGAG	90
Db	1663	AAGCAGGGGGGAACGCTGGACGACCTTAGAG	1692
RESULT 10			
AAX79304			
ID	AAX79304	standard; cDNA; 2268 BP.	
XX	AAX79304;		
AC			
XX			
DT	31-AUG-1999	(first entry)	
XX			
DE	Human IKK-beta coding sequence.		
XX			
KW	Human; IKK-beta; I-Kappa B-Kinase; inhibitory protein; diagnosis; NF-kB;		
KW	Nuclear Factor Kappa B; interaction; binding target; ds.		
XX			
OS	Homo sapiens.		
XX			
EN	US5916760-A.		
XX			
PD	29-JUN-1999.		
XX			
PF	17-JUN-1998; 98US-00099125.		
XX			
PR	01-JUL-1997; 97US-00887114.		
PR	10-JUL-1997; 97US-00890853.		
XX			
PA	(TULA-) TULARIK INC.		
XX			
PI	Goeddel DV, Woronicz J;		
XX			
DR	WPI; 1999-384722/32.		
DR	P-PSDB; AAY14515.		
XX			
PT	Screening for agents which modulate the interaction of IKK-beta		
PT	polypeptides and their binding targets.		
XX			
PS	Claim 4; Col 11-14; 14pp; English.		
XX			
CC	This sequence represents the coding region for human IKK-beta, a novel		
CC	IKB Kinase (I-Kappa B-Kinase, one of a family of inhibitory proteins		
CC	which interact with Nuclear Factor Kappa B (NF-kB)). The invention		
CC	relates to a method of screening for agents which modulate the		
CC	interaction of human IKK-beta polypeptides and their binding targets.		
CC	Agents which modulate the IKK-beta binding are useful in a variety of		
CC	diagnostic and therapeutic applications where the disease is associated		
CC	with improper utilization of a pathway involving IKK-beta proteins (e.g.		
CC	NF-kB activation and IKK-beta-dependent transcriptional activation)		
XX			
SQ	Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;		
Query Match	100.0%;	Score 90; DB 2; Length 2268;	
Best Local Similarity	100.0%;	Pred. No. 1.7e-19;	
Matches	90; Conservative	0; Mismatches	0; Indels
			0; Gaps
			0;
QY	1	GAACGATCATCGCTCTGCAGACCGACACATTGTGGACTTTACAGAGGAGCCCCCATGGCGCGG	60
Db	1603	GAACGATCATCGCTCTGCAGACCGACACATTGTGGACTTTACAGAGGAGCCCCCATGGCGCGG	1662
QY	61	AAGCAGGGGGGAACGCTGGACGACCTTAGAG	90
Db	1663	AAGCAGGGGGGAACGCTGGACGACCTTAGAG	1692
RESULT 11			
AAC81425			

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; eczema; arthritis; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX FH 2203..2235
 XX CDS /*tag= a
 XX /*product= "IKKbeta peptide"

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX P-PSDB; AAM48506.

XX Novel antiinflammatory compound comprising membrane translocation domain
 fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
 activation, and for treating asthma, lung inflammation, psoriasis.

XX Disclosure; Page; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 AAM4828-AAM48645), comprising a membrane translocation domain (AAM48620-
 AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
 residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
 antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
 antirheumatic, antiarthritic, osteopathic, antibacterial,
 immunosuppressive, dermatological, neuroprotective, nootropic,
 antiatherosclerotic, virucide and anti-allergic activity. The compounds
 act as selective inhibitors of cytokine-mediated NFkappaB activation by
 blocking interaction of IkkappaB kinase beta (IKKbeta) at the NEMO binding
 domain that results in inhibition of IKKbeta kinase activation and
 subsequent decreased phosphorylation of IkkappaB. The compounds are useful
 for treating inflammatory disorders, e.g. asthma, lung inflammation or
 cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
 bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
 lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
 transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
 viral infections; and ataxia telangiectasia. The compounds are also
 useful for treating pro-inflammatory responses such as allergies,
 urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
 sunburn, aging and arthritis. Note: The present sequence is not given in
 the printed specification but is that of human IKKbeta encoding
 polynucleotide derived from the sequence given at GenBank Number AR067807

XX Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 6; Length 2268;

Best Local Similarity 100.0%; Pred. No. 1.7e-19;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCG 60

Db 1603 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCG 1662

QY 61 AAGCAGGGGGACGCTGGACGACCTAGAG 90

Db 1663 AAGCAGGGGGACGCTGGACGACCTAGAG 1692

RESULT 13

ABX11974

ID ABX11974 standard; cDNA; 2268 BP.

XX AC ABX11974;

XX 08-MAY-2003 (first entry)

XX Human IKK-alpha related cDNA.

XX Human; gene; ss; inhibitor of nuclear factor kappa-B kinase alpha;
 KW IKK-alpha; conserved helix-loop-helix ubiquitous kinase; CHUK; IKK-alpha;
 KW nuclear factor kappa B; NF-kappaB; cell regulation; IKK; phosphorylation;
 KW IkkappaB; signal transduction disorder; genetic defect;
 KW autoimmune disease; neuroprotective; immunostimulant.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..2268
 XX /*tag= a
 XX /*product= "IKK-alpha related polypeptide"

XX US6479266-B1.

XX 12-NOV-2002.

XX 02-JUL-1998; 98US-00109986.

XX 01-JUL-1997; 97US-00887115.

XX 10-JUL-1997; 97US-00890854.

XX (TULA-) TULARIK INC.

XX Rothe M, Cao Z, Regnier C;

XX WPI; 2003-238112/29.

XX P-PSDB; ABG75804.

XX New isolated IKK polypeptide involved in transcription factor activation,
 useful for diagnosing and treating disorders with aberrant activity of
 the IKK polypeptide, such as signal transduction disorders and genetic
 defects.

XX Disclosure; Col 13-16; 15pp; English.

XX The invention discloses methods and compositions relating to isolated
 inhibitor of nuclear factor kappa-B kinase alpha (IKK-alpha), also known
 as the conserved helix-loop-helix ubiquitous kinase (CHUK), polypeptides.
 CC IKK-alpha polypeptides regulate nuclear factor kappa B (NF-kappaB)
 CC activation and hence regulate cell function. Also disclosed are methods
 CC for screening for an agent which modulates the interaction of an IKK
 CC polypeptide to a binding target and for screening for an agent which
 CC modulates the ability of an IKK polypeptide to specifically phosphorylate
 CC an IkkappaB polypeptide. The methods and compositions of the present
 CC invention are useful for the diagnosis and treatment of disorders
 CC associated with the aberrant activity of the IKK polypeptide, such as
 CC signal transduction disorders, genetic defects and autoimmune diseases.
 CC The sequence presented is the human IKK-alpha related cDNA

XX Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 7; Length 2268;

Best Local Similarity 100.0%; Pred. No. 1.7e-19;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCG 60

Db 1603 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCG 1662

QY 61 AAGCAGGGGGACGCTGGACGACCTAGAG 90

Db	1663	AAGCAGGGGGGAACGCTGGACGACCTAGAG	1692
DT	XX	24-JUL-1998	(first entry)
DE	XX	DNA encoding inhibitory subunit I-kappa-B signalosome kinase 2.	
XX	XX	Inhibitory subunit; I-kappa-B-beta; nuclear factor kappa-B;	
KW	KW	NF-kappa-B/Rel dimer; inhibitory activity; phosphorylation;	
KW	KW	stimulus-inducible I-kappa-B kinase; IKK; signalosome; I-kappa-B-alpha;	
KW	KW	identification; stimulate; signal transduction; the NF-kappa-B cascade;	
KW	KW	therapeutic composition; inflammatory; neurodegenerative; disease;	
KW	KW	autoimmune disease; cancer; ss.	
XX	XX	Homo sapiens.	
OS	XX		
XX	XX	Key	Location/Qualifiers
FT	FT	CDS	1..2271
FT	FT		/*tag= a
XX	XX	WO9808955-A1.	
XX	XX	05-MAR-1998.	
PD	PD		
XX	XX	26-AUG-1997;	97WO-US015003.
PF	PF		
XX	XX	26-AUG-1996;	96US-00697393.
PR	PR	13-AUG-1997;	97US-00910820.
XX	XX	(SIGN-) SIGNAL PHARM INC.	
PA	PA		
XX	XX	Mercurio F, Zhu H, Barbosa M, Li G, Murray BW;	
PI	PI	WPI; 1998-179440/16.	
XX	XX	P-PSDB; AAW56328.	
DR	DR		
XX	XX	New isolated stimulus-inducible I-kappa-B kinase signalosome - useful for	
PT	PT	developing products for treating, e.g. inflammatory neuro-degenerative	
PT	PT	and auto-immune diseases.	
XX	XX	Disclosure; Page 58-60; 115pp; English.	
PS	PS		
XX	XX	The present sequence encodes an inhibitory subunit I-kappa-B kinase (IKK)	
CC	CC	2. IKK kinases, when incorporated into an IKK signalosome, are capable of	
CC	CC	phosphorylating inhibitory subunit I-kappa-B-alpha, at serine residues 32	
CC	CC	and 36. I-kappa-B-alpha retains nuclear factor (NF) kappa-B in the	
CC	CC	cytoplasm. I-kappa-B proteins contain 5-7 ankyrin-like repeats which are	
CC	CC	required for association with the NF-kappa-B/Rel dimer and for inhibitory	
CC	CC	activity. A stimulus-inducible IKK "signalosome" is described that is	
CC	CC	capable of specifically phosphorylating I-kappa-B-alpha at residues S32	
CC	CC	and S36, without the addition of exogenous cofactors. The proteins of the	
CC	CC	invention can be used to identify agents that inhibit or stimulate signal	
CC	CC	transduction via the NF-kappa-B cascade. Therapeutic compositions	
CC	CC	comprising such agents may be used for treating a patient afflicted with	
CC	CC	a disorder associated with the activation of an IKK signalosome. The	
CC	CC	agents may be used to treat, e.g. inflammatory, neurodegenerative	
CC	CC	diseases and autoimmune diseases, cancer and viral infections. The	
CC	CC	antibodies may be used in a kit for detecting IKK signalosome activity in	
CC	CC	a sample	
XX	XX	Sequence 2271 BP; 604 A; 569 C; 661 G; 437 T; 0 U; 0 Other;	
SQ	SQ		
		Query Match	100.0%; Score 90; DB 2; Length 2271;
		Best Local Similarity	100.0%; Pred. No. 1.7e-19;
		Matches	90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCCCGG	60
Db	1603	GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCCCGG	1662
QY	61	AAGCAGGGGGGAACGCTGGACGACCTAGAG	90
Db	1663	AAGCAGGGGGGAACGCTGGACGACCTAGAG	1692
		Search completed: September 23, 2004, 19:55:55	

Db	1663	AAGCAGGGGGGAACGCTGGACGACCTAGAG	1692
RESULT 14			
ACD66625			
ID	ACD66625	standard; cDNA; 2268 BP.	
XX	ACD66625;		
AC	AC		
XX	16-SEP-2003	(first entry)	
DT	XX	Human inhibitor-kappa B kinase-beta DNA sequence.	
DE	XX		
XX	XX	Human; inhibitor-kappa B kinase-beta; anorectic; antidiabetic;	
KW	KW	antiinflammatory; cytostatic; gene therapy; antisense compound; obesity;	
KW	KW	diabetes type II; inflammatory disorder; cancer; leukaemia; gene; ss.	
XX	XX	Homo sapiens.	
OS	XX		
XX	XX	US2003050270-A1.	
PN	PN		
XX	XX	13-MAR-2003.	
PD	PD		
XX	XX	24-MAY-2002; 2002US-00156610.	
PF	PF		
XX	XX	20-NOV-1998; 98US-00197008.	
PR	PR	28-JUL-1999; 99WO-US016959.	
XX	XX	30-AUG-2001; 2001US-00856246.	
XX	XX	(MONI/) MONIA B P.	
PA	PA	(COWS/) COWSERT L M.	
XX	XX	(KOLL/) KOLLER E.	
PI	PI	Monia BP, Cowsert LM, Koller E;	
XX	XX	WPI; 2003-512357/48.	
DR	DR	P-PSDB; ABO32508.	
XX	XX	New antisense compound, useful for preparing a composition for treating	
PT	PT	obesity, diabetes type II, inflammatory disorder or cancer e.g.,	
PT	PT	leukemia.	
XX	XX	Example 13; Page 29-31; 49pp; English.	
PS	PS		
XX	XX	The invention describes a new antisense compound, which is 8-30	
CC	CC	nucleobases in length targeted to a nucleic acid molecule encoding	
CC	CC	inhibitor-kappa B Kinase-beta that specifically hybridises with and	
CC	CC	inhibits the expression of inhibitor-kappa B Kinase-beta. The compound is	
CC	CC	useful for preparing a composition for treating obesity, diabetes type	
CC	CC	II, inflammatory disorder or cancer e.g., leukaemia. This sequence	
CC	CC	represents human inhibitor-kappa B kinase-beta DNA	
XX	XX	Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;	
SQ	SQ		
		Query Match	100.0%; Score 90; DB 8; Length 2268;
		Best Local Similarity	100.0%; Pred. No. 1.7e-19;
		Matches	90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCCCGG	60
Db	1603	GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCCCGG	1662
QY	61	AAGCAGGGGGGAACGCTGGACGACCTAGAG	90
Db	1663	AAGCAGGGGGGAACGCTGGACGACCTAGAG	1692
RESULT 15			
AAV22842			
ID	AAV22842	standard; DNA; 2271 BP.	
XX	XX		
AC	AC		
XX	AAV22842;		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 14:33:31 ; Search time 2490 Seconds
(without alignments)
1079.356 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080

Perfect score: 90

Sequence: 1 gaacggtatgctctgca.....gaacgtggacacactagag 90

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	588	12	BG336659 602405777
2	90	100.0	589	12	BG107446 602277558
3	90	100.0	727	10	BE384533 601277926
4	90	100.0	745	12	BI084392 602869515

5	90	100.0	868	14	CD251031
6	90	100.0	944	13	BU857051
7	90	100.0	974	13	BQ669894
c 8	90	100.0	1201	9	AL542182
c 9	88.4	98.2	878	13	BQ877352
c 10	86.8	96.4	557	10	BF590924
c 11	86	95.6	402	10	BE077902
c 12	86	95.6	501	28	AQ827088
c 13	86	95.6	864	14	CD299893
c 14	81.6	90.7	400	9	AI906358
c 15	79	87.8	401	10	AW997999
c 16	78	86.7	736	14	CA429223
c 17	78	86.7	789	10	BE734952
c 18	77.2	85.8	558	12	BI296436
c 19	77.2	85.8	558	12	BI296613
c 20	77.2	85.8	565	12	BI291377
c 21	77.2	85.8	714	14	CF113406
c 22	76.4	84.9	946	13	BU558245
c 23	74	82.2	575	12	BG087220
c 24	74	82.2	738	14	CF537632
c 25	74	82.2	741	10	BE310997
c 26	74	82.2	765	14	CD805176
c 27	74	82.2	943	13	BU511732
c 28	74	82.2	2193	11	BC004772
c 29	71	78.9	302	10	BF916026
c 30	69.8	77.6	465	10	AW656805
c 31	69.6	77.3	559	9	AA128064
c 32	69.2	76.9	732	13	BY764258
c 33	68.2	75.8	390	12	BI976355
c 34	68.2	75.8	506	10	BF602600
c 35	68	75.6	393	9	AI906367
c 36	67.4	74.9	300	10	BF915824
c 37	66.2	73.6	718	10	BE687229
c 38	62.4	69.3	949	12	BG476715
c 39	62	68.9	342	10	BF834440
c 40	55.4	61.6	703	13	BU475878
c 41	54.6	60.7	622	12	BM489568
c 42	54.6	60.7	690	13	BU372250
c 43	54.6	60.7	780	13	BU373892
c 44	47.8	53.1	958	14	CA981256
c 45	43	47.8	616	10	AW955375

ALIGNMENTS

RESULT 1	BG336659	588 bp	linear	EST 27-FEB-2001
LOCUS	602405777F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4543218 5',			
DEFINITION	RNA sequence.			
ACCESSION	BG336659			
VERSION	BG336659.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 588)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Clone Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1224 row: j column: 19 High quality sequence stop: 588.			

FEATURES
source

Location/Qualifiers
1. .588
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4543218"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 90; DB 12; Length 588;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 60
|||||
Db 459 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 518
QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
|||||
Db 519 AAGCAGGGGGGAACGCTGGACGACCTAGAG 548

RESULT 2

BG107446 589 bp mRNA linear EST 30-JAN-2001
LOCUS 602277538F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4365254 5',
DEFINITION mRNA sequence.
ACCESSION BG107446
VERSION BG107446.1 GI:12601292
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 589)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LLAM10014 row: c column: 15
High quality sequence stop: 419.

FEATURES
source

Location/Qualifiers
1. .589
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4365254"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 90; DB 12; Length 589;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 60
|||||
Db 42 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 101
QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
|||||
Db 102 AAGCAGGGGGGAACGCTGGACGACCTAGAG 131
RESULT 3
BE384533 727 bp mRNA linear EST 21-JUL-2000
LOCUS 601277926F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618751 5',
DEFINITION mRNA sequence.
ACCESSION BE384533
VERSION BE384533.1 GI:9329898
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 727)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/BTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LLCW288 row: c column: 08
High quality sequence stop: 614.

FEATURES
source

Location/Qualifiers
1. .727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3618751"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 90; DB 10; Length 727;
Best Local Similarity 100.0%; Pred. No. 7.8e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 60
|||||
Db 356 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 415
QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
|||||
Db 416 AAGCAGGGGGGAACGCTGGACGACCTAGAG 445

```

RESULT 4
BI084392      745 bp      mRNA      linear      EST 20-JUN-2001
LOCUS        602869515F1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5014442 5',
DEFINITION   mRNA sequence.
ACCESSION    BI084392
VERSION      BI084392.1 GI:14502722
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 745)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: CLONETECH Laboratories, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1821 row: m column: 03
              High quality sequence stop: 744.
              Location/Qualifiers
                source          1..745
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5014442"
                /tissue_type="epidermoid carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_102"
                /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Library constructed
                by Ling Hong in the laboratory of Gerald M. Rubin
                (University of California, Berkeley) using ZAP-cDNA
                synthesis kit (Stratagene) and Superscript II RT (Life
                Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match      100.0%; Score 90; DB 12; Length 745;
Best Local Similarity 100.0%; Pred. No. 7.8e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCACACCGACATTGTGGACTTACAGAGAGCCCATGGCGCG 60
    |||||||
Db 180 GAACGGATGATGGCTCTGCACACCGACATTGTGGACTTACAGAGAGCCCATGGCGCG 239
    |||||||

Qy 61 AAGCAGGGGGGAACGCTGGAGCCTAGAG 90
    |||||||
Db 240 AAGCAGGGGGGAACGCTGGAGCCTAGAG 269

RESULT 5
CD251031      868 bp      mRNA      linear      EST 22-MAY-2003
LOCUS        AGENCOURT_14214315 NIH_MGC_179 Homo sapiens cDNA clone
DEFINITION   IMAGE:30385244 5', mRNA sequence.
ACCESSION    CD251031
VERSION      CD251031.1 GI:31011497
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 868)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.

```

```

TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Dr. Michael Brownstein
              CDNA Library Preparation: Invitrogen Corp
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: NDAM451 row: p column: 21
              High quality sequence stop: 687.
              Location/Qualifiers
                source          1..868
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:30385244"
                /tissue_type="Pituitary"
                /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                /clone_lib="NIH_MGC_179"
                /note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV
                (destroyed); Site_2: NotI; Library is oligo-dT primed and
                directionally cloned (EcoRV site is destroyed upon
                cloning). Average insert size 1.1 kb. Library was
                constructed by (Invitrogen). Note: this is a NIH_MGC
                Library."

ORIGIN
Query Match      100.0%; Score 90; DB 14; Length 868;
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCACACCGACATTGTGGACTTACAGAGAGCCCATGGCGCG 60
    |||||||
Db 101 GAACGGATGATGGCTCTGCACACCGACATTGTGGACTTACAGAGAGCCCATGGCGCG 160
    |||||||

Qy 61 AAGCAGGGGGGAACGCTGGAGCCTAGAG 90
    |||||||
Db 161 AAGCAGGGGGGAACGCTGGAGCCTAGAG 190

RESULT 6
BU857051      944 bp      mRNA      linear      EST 16-OCT-2002
LOCUS        AGENCOURT_10480781 NIH_MGC_107 Homo sapiens cDNA clone
DEFINITION   IMAGE:6646854 5', mRNA sequence.
ACCESSION    BU857051
VERSION      BU857051.1 GI:24042041
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 944)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Rubin Laboratory
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2886 row: f column: 06
              High quality sequence stop: 718.

```

FEATURES
source

Location/Qualifiers
1. .944
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6646854"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 90; DB 13; Length 944;
Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCCG 60
|||||
Db 213 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCCG 272
QY 61 AAGCAGGGGGGACGCTGGACGACCTAGAG 90
|||||
Db 273 AAGCAGGGGGGACGCTGGACGACCTAGAG 302

RESULT 7
BQ669894

LOCUS BQ669894 974 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT.8184827 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257524
5', mRNA sequence.
ACCESSION BQ669894
VERSION BQ669894.1 GI:21780728
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2411 row: p column: 05
High quality sequence stop: 527.

FEATURES
source

Location/Qualifiers
1. .974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6257524"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin

ORIGIN

Query Match 100.0%; Score 90; DB 13; Length 974;
Best Local Similarity 100.0%; Pred. No. 8.6e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCCG 60
|||||
Db 178 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCCG 237
QY 61 AAGCAGGGGGGACGCTGGACGACCTAGAG 90
|||||
Db 238 AAGCAGGGGGGACGCTGGACGACCTAGAG 267

RESULT 8

AL542182/c
LOCUS AL542182 1201 bp mRNA linear EST 12-MAY-2003
DEFINITION AL542182 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE008YML7
3-PRIME, mRNA sequence.
ACCESSION AL542182
VERSION AL542182.2 GI:30547081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12873974.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4655.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE008AG09NP1&cluster=4655.r. Contact :
Peng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE008AG09NP1.

FEATURES
source

Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE008YML7"
/tissue_type="PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 100.0%; Score 90; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 9.2e-15;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCCG 60
|||||
Db 658 GAACGGATGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCCG 599
QY 61 AAGCAGGGGGGACGCTGGACGACCTAGAG 90
|||||
Db 598 AAGCAGGGGGGACGCTGGACGACCTAGAG 569

(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."


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RESULT 9
BO877352
LOCUS
DEFINITION BO877352 878 bp mRNA linear EST 16-AUG-2002
5', mRNA sequence.
AGENCOURT_8072483 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084011
BO877352
VERSION BO877352.1 GI:22269360
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nhl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLGW2315 row: b column: 12
High quality sequence stop: 621.
FEATURES
source
1..878
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6084011"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTE7; Site:1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN
Query Match 98.2%; Score 88.4; DB 13; Length 878;
Best Local Similarity 98.9%; Pred. No. 2.3e-14;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAACGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCCATGGGCCGG 60
Db 551 GAACGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCCATGGGCCGG 610
QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 611 AAGCAGGGGGGAACGCTGGACGACCTAAAG 640
RESULT 10
BF590924/c
LOCUS
DEFINITION BF590924 557 bp mRNA linear EST 12-DEC-2000
7b46b08.x1 NCI_CGAP Col6 Homo sapiens cDNA clone IMAGE:3318999 3',
similar to TR:075327 075327 1KB KINASE BETA SUBUNIT. [1] ;, mRNA
sequence.
BF590924
VERSION BF590924.1 GI:11683248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE 20202663
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 557)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 402.
FEATURES
source
1..557
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3318999"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Col6"
/note="Organ: colon; Vector: p77T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351)
Subtraction by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match 96.4%; Score 86.8; DB 10; Length 557;
Best Local Similarity 97.8%; Pred. No. 5.5e-14;
Matches 88; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAACGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCCATGGGCCGG 60
Db 332 GAACGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCCATGGGCCGG 273
QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 272 AAGCAGGGGGGAACGCTGGACCTAGAG 243
RESULT 11
BE077902
LOCUS
DEFINITION BE077902 402 bp mRNA linear EST 09-JUN-2000
CM1-BT0614-110300-142-c10 BT0614 Homo sapiens cDNA, mRNA sequence.
BE077902
ACCESSION BE077902
VERSION BE077902.1 GI:8429180
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE 20202663

```


/clone="IMAGE:30388043"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /clone_lib="NIH_MGC_180"
 /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
 Site 2: EcoRV (destroyed); Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.68 kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 95.6%; Score 86; DB 14; Length 864;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGATGATGCTCTGCAGACGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 60
 |||||
 Db 221 GAACGATGATGCTCTGCAGACGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 280
 |||||

QY 61 AAGCAGGGGGAGCGCTGGACGACCT 86
 Db 281 AAGCAGGGGGAGCGCTGGACGACCT 306

RESULT 14

AI906358 400 bp mRNA linear EST 30-MAR-2000
 LOCUS RC-BT108-040399-031 BT108 Homo sapiens cDNA, mRNA sequence.

DEFINITION AI906358
 ACCESSION AI906358
 VERSION AI906358.1 GI:6496745
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 400)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT108-031.html
 &t3=040399&t4=1)

Seq primer: puc 18 forward.
 Location/Qualifiers

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Adult"
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 /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
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 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 90.7%; Score 81.6; DB 9; Length 400;
 Best Local Similarity 95.5%; Pred. No. 1.4e-12;
 Matches 84; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 Db 1 ACGGATGATGGCTCTGCAGACGACATTGTGGACTTACAGAGGAGCCCATGGGCGGAA 60
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QY 63 GCAGGGGGGAAACGCTGGACGACCTAGAG 90
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 Db 61 GCAGGGGGGAAACGCTGGACGACCTAGAG 88
 |||||

RESULT 15

AW997999 401 bp mRNA linear EST 05-JUN-2000
 LOCUS RCL-BN0056-230200-021-b11 BN0056 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW997999
 ACCESSION AW997999
 VERSION AW997999.1 GI:8258233
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 401)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=RCL-BN0056-230
 200-021-b11&t3=2000-02-23&t4=1)

Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 401.
 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BN0056"
 /note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 87.8%; Score 79; DB 10; Length 401;
 Best Local Similarity 98.9%; Pred. No. 7.3e-12;

Matches	90;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
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Db	43	GAACGGATGATGGCTCTGCAGAACCGACATTGTGGACTTACAGAGGAGCCCCCATGGGCG	102						
Qy	60	GAAGCAGGGGGGAACGCTGGACGACCTAGAG	90						
Db	103	GAAGCAGGGGGGAACGCTGGACGACCTAGAG	133						

Search completed: September 23, 2004, 21:02:15
 Job time : 2495 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 19:41:56 ; Search time 369 Seconds
(without alignments)
135.354 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080

Perfect score: 90

Sequence: 1 gaacggatgatgctctgca.....gaacgtggacgacctagag 90

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	90	100.0	1055	3	US-09-215-131-3
2	90	100.0	1055	3	US-09-222-734-3
3	90	100.0	2268	2	US-08-890-853-1
4	90	100.0	2268	2	US-09-099-125A-1
5	90	100.0	2268	2	US-09-099-124A-1
6	90	100.0	2268	2	US-09-197-008-1
7	90	100.0	2268	3	US-09-032-476-1
8	90	100.0	2268	3	US-08-890-854-1
9	90	100.0	2268	3	US-09-023-324-1
10	90	100.0	2268	4	US-09-109-986-1
11	90	100.0	2271	3	US-08-910-820-8
12	90	100.0	2271	4	US-09-844-908-8
13	90	100.0	2931	3	US-09-168-629-14
14	90	100.0	3966	3	US-09-215-131-1
15	90	100.0	3966	3	US-09-222-734-1
16	35.6	39.6	1874	4	US-09-536-882A-6
17	35.6	39.6	2025	3	US-09-160-483-2
18	35.6	39.6	3314	4	US-09-536-882A-5
19	34.6	38.4	2146	3	US-09-032-476-5
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21	34.6	38.4	2146	3	US-09-023-324-5
22	34.6	38.4	2146	4	US-09-109-986-5
23	34.6	38.4	2238	2	US-08-890-853-3
24	34.6	38.4	2238	2	US-09-099-125A-3
25	34.6	38.4	2238	2	US-09-099-124A-3
26	34.6	38.4	2238	3	US-09-032-476-3
27	34.6	38.4	2238	3	US-08-890-854-3

28	34.6	38.4	2238	3	US-09-023-324-3	Sequence 3, Appli
29	34.6	38.4	2238	4	US-09-109-986-3	Sequence 3, Appli
30	34.6	38.4	2251	3	US-08-910-820-7	Sequence 7, Appli
31	34.6	38.4	2251	4	US-09-844-908-7	Sequence 7, Appli
32	34.6	38.4	2273	3	US-09-168-629-1	Sequence 1, Appli
33	34.6	38.4	2273	3	US-08-810-131A-1	Sequence 1, Appli
34	33	36.7	2273	2	US-09-197-360-1	Sequence 1, Appli
35	33	36.7	2273	4	US-09-856-074B-1	Sequence 1, Appli
36	33	36.7	2273	4	US-09-417-197-120	Sequence 122, App
37	33	36.7	2294	4	US-09-417-197-120	Sequence 120, App
38	30.2	33.6	909	4	US-09-252-991A-15957	Sequence 15957, A
39	30.2	33.6	1221	4	US-09-252-991A-16324	Sequence 16324, A
40	29.2	32.4	1074	2	US-08-463-081B-29	Sequence 29, Appl
41	29.2	32.4	1074	2	US-08-461-379A-29	Sequence 29, Appl
42	29.2	32.4	1074	2	US-08-462-390B-29	Sequence 29, Appl
43	29.2	32.4	1074	3	US-08-463-074B-29	Sequence 29, Appl
44	29.2	32.4	1074	3	US-08-455-585C-29	Sequence 29, Appl
45	29.2	32.4	1074	3	US-08-652-446-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-09-215-131-3
; Sequence 3, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
; FILE REFERENCE: 1449.002
; CURRENT APPLICATION NUMBER: US/09/215,131
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: human
US-09-215-131-3

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Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAACGGATGCTCTGCGAGACCGCATTTGGACTTACAGAGAGCCCCATGGGCCGG 60
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QY	61	AAGCGGGGGGAACGCTGGACGACCTAGAG 90
DB	382	AAGCGGGGGGAACGCTGGACGACCTAGAG 411

RESULT 2

US-09-222-734-3
; Sequence 3, Application US/09222734A
; Patent No. 6077701
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
; FILE REFERENCE: 12441.78080
; CURRENT APPLICATION NUMBER: US/09/222,734A
; CURRENT FILING DATE: 1998-12-29
; EARLIER APPLICATION NUMBER: 09/215,131
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 60/068,954
; EARLIER FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

US-08-890-853-1
; Sequence 1, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/890,853
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-890-853-1

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Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 AAGCAGGGGGAACGCTGGACGACCTAGAG 90
Db 382 AAGCAGGGGGAACGCTGGACGACCTAGAG 411

RESULT 3
US-08-890-853-1
; Sequence 1, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/890,853
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-890-853-1

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Best Local Similarity 100.0%; Pred. No. 2e-20;
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Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCCGG 1662
QY 61 AAGCAGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 4

US-09-099-125A-1
; Sequence 1, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/099,125A
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-099-125A-1

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Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 AAGCAGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 5
US-09-099-124A-1
; Sequence 1, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/099,124A
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-099-124A-1

RESULT 4

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-099-124A-1

Query Match 100.0%; Score 90; DB 2; Length 2268;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 1662

Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 6
US-09-197-008-1
; Sequence 1, Application US/09197008
; Patent No. 5977341
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
; FILE REFERENCE: RTS-0019
; CURRENT APPLICATION NUMBER: US/09/197,008
; CURRENT FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2268)
; US-09-197-008-1

Query Match 100.0%; Score 90; DB 2; Length 2268;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 1662

Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692

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RESULT 7
US-09-032-476-1
; Sequence 1, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-032-476-1

Query Match 100.0%; Score 90; DB 3; Length 2268;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCGG 60
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Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 8
US-08-890-854-1
; Sequence 1, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO

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; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-890-854-1

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Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
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RESULT 9
US-09-023-324-1
; Sequence 1, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-109-986-1

Query Match 100.0%; Score 90; DB 4; Length 2268;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
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RESULT 10
US-09-109-986-1
; Sequence 1, Application US/09109986
; Patent No. 6479266
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-109-986-1

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Best Local Similarity 100.0%; Pred. No. 2e-20;
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RESULT 12
US-09-844-908-8
; Sequence 8, Application US/09844908
; Patent No. 6576437
; GENERAL INFORMATION:

RESULT 13
US-09-168-629-14
Sequence 14, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DIDONATO, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zand, Ebrahim
TITLE OF INVENTION: IxB Kinase, Sub
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/1-08
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061.
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(2306)
US-09-168-629-14

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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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RESULT 14
US-09-215-131-1
; Sequence 1, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
; FILE REFERENCE: 1449.002
; CURRENT APPLICATION NUMBER: US/09/215,131
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3966
; TYPE: DNA
; ORGANISM: human
US-09-215-131-1

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Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
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Query Match      100.0%; Score 90; DB 3; Length 3966;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db 1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
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RESULT 15
US-09-222-734-1
; Sequence 1, Application US/09222734A
; Patent No. 6077701
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
; FILE REFERENCE: 12441.78080
; CURRENT APPLICATION NUMBER: US/09/222,734A
; CURRENT FILING DATE: 1998-12-29
; EARLIER APPLICATION NUMBER: 09/215,131
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 60/068,954
; EARLIER FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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Searched: 3337386 seqs, 2532474682 residues

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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	90	100.0	1558	15	Sequence 24344, A
3	90	100.0	2268	10	US-10-106-698-455
4	90	100.0	2268	15	Sequence 455, App
5	90	100.0	2268	15	US-09-847-946A-1
6	90	100.0	2268	15	Sequence 1, Appli
7	90	100.0	2271	9	US-10-156-610-1
8	90	100.0	2271	9	US-10-243-408-1
9	90	100.0	2271	9	US-09-844-908-8
10	90	100.0	2271	15	Sequence 8, Appli
11	86	95.6	81099	13	US-10-338-462-8
12	77.2	85.8	3038	13	US-09-796-872-1
13	74	82.2	2274	15	US-10-087-192-1757
14	74	82.2	3210	13	US-10-087-192-1756

15	70	77.8	67076	13	US-10-087-192-1753	Sequence 1753, Appl
16	35.6	39.6	1875	15	US-10-188-937A-6	Sequence 6, Appli
17	35.6	39.6	3314	15	US-10-188-937A-5	Sequence 5, Appli
18	34.6	38.4	2146	15	US-10-243-408-5	Sequence 5, Appli
19	34.6	38.4	2238	15	US-10-243-408-3	Sequence 3, Appli
20	34.6	38.4	2251	9	US-09-844-908-7	Sequence 7, Appli
21	34.6	38.4	2251	9	US-09-844-988-7	Sequence 7, Appli
22	34.6	38.4	2251	15	US-10-338-462-7	Sequence 1, Appli
23	34.6	38.4	2273	9	US-09-796-872-1	Sequence 632, App
24	34.6	38.4	3525	15	US-10-101-510-632	Sequence 91, Appl
25	34.6	38.4	3618	17	US-10-741-601-91	Sequence 5639, Ap
26	33.6	37.3	53328	17	US-10-741-601-5639	Sequence 1, Appli
27	33	36.7	2273	15	US-10-145-857-1	Sequence 122, App
28	33	36.7	2291	15	US-10-072-036-122	Sequence 120, App
29	33	36.7	2294	15	US-10-072-036-120	Sequence 115364, App
30	30.6	34.0	649	13	US-10-027-632-115364	Sequence 115365, App
31	30.6	34.0	649	13	US-10-027-632-115365	Sequence 115366, App
32	30.6	34.0	649	13	US-10-027-632-115366	Sequence 115366, App
33	30.6	34.0	649	16	US-10-027-632-115364	Sequence 115364, App
34	30.6	34.0	649	16	US-10-027-632-115365	Sequence 115365, App
35	30.6	34.0	649	16	US-10-027-632-115366	Sequence 115366, App
36	30.6	34.0	715	13	US-10-425-114-18909	Sequence 18909, A
37	30.6	34.0	993	17	US-10-389-566-188	Sequence 188, App
38	30.2	33.6	1087	17	US-10-437-963-44491	Sequence 44491, A
39	30.2	33.6	1754	17	US-10-437-963-44490	Sequence 44490, A
40	29.8	33.1	3471	16	US-10-369-493-45054	Sequence 45054, A
41	29.4	32.7	366	15	US-10-156-761-2009	Sequence 2009, Ap
42	29.4	32.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
43	29.2	32.4	780	17	US-10-437-963-3953	Sequence 3953, App
44	29.2	32.4	1077	11	US-09-826-509-558	Sequence 558, App
45	29.2	32.4	1345	9	US-09-853-450-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-918-995-24344
; Sequence 24344, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24344
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(506)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24344

Query Match 100.0%; Score 90; DB 10; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AAGCAGGGGGAACGCTGGACGACCTAGAG	90
DB	124	AAGCAGGGGGAACGCTGGACGACCTAGAG	153

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US-10-106-698-455
; Sequence 455, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 455
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (420)..(420)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-455

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Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACACCTAGAG 90
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RESULT 3
US-09-847-946A-1
; Sequence 1, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkel, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:wild-type IKK
; OTHER INFORMATION: NED
US-09-847-946A-1

Query Match          100.0%; Score 90; DB 10; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 60
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QY 61 AAGCAGGGGGGAACGCTGGACACCTAGAG 90
Db 877 AAGCAGGGGGGAACGCTGGACACCTAGAG 906

RESULT 4
US-10-156-610-1
; Sequence 1, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
; FILE REFERENCE: ISPH-0666
; CURRENT APPLICATION NUMBER: US/10/156,610
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/856,246
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US99/16959
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/197,008
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2268)
US-10-156-610-1

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Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCAGGGGGGAACGCTGGACACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACACCTAGAG 1692

RESULT 5
US-10-243-408-1
; Sequence 1, Application US/10243408
; Publication No. US20030077683A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 60
Db 1603 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 1662

QY 61 AAGCAGGGGGGAACGCTGGACACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACACCTAGAG 1692
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RESULT 4
US-10-156-610-1
; Sequence 1, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
; FILE REFERENCE: ISPH-0666
; CURRENT APPLICATION NUMBER: US/10/156,610
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/856,246
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US99/16959
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/197,008
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2268)
US-10-156-610-1
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Query Match          100.0%; Score 90; DB 15; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 60
Db 1603 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCATGGGCGG 1662

QY 61 AAGCAGGGGGGAACGCTGGACACCTAGAG 90
Db 1663 AAGCAGGGGGGAACGCTGGACACCTAGAG 1692
```

```
RESULT 5
US-10-243-408-1
; Sequence 1, Application US/10243408
; Publication No. US20030077683A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,408
FILING DATE: 13-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/890,854
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-243-408-1

Query Match 100.0%; Score 90; DB 15; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGCGG 60
Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGCGG 1662
Qy 61 AAGCAGGGGGGAGCGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGAGCGCTGGACGACCTAGAG 1692

RESULT 6
US-09-844-908-8
Sequence 8, Application US/09844908
Patent No. US20020151021A1
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
Zhu, Hengyi
Barbosa, Miguel
Li, Gian
Murray, Brion W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2271 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-844-908-8
Query Match 100.0%; Score 90; DB 9; Length 2271;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGCGG 60
Db 1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGCGG 1662
Qy 61 AAGCAGGGGGGAGCGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGAGCGCTGGACGACCTAGAG 1692

RESULT 7
US-09-844-988-8
Sequence 8, Application US/09844988
Patent No. US20020158764A1
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
Zhu, Hengyi
Barbosa, Miguel
Li, Gian
Murray, Brion W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,988
FILING DATE: 26-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,820
FILING DATE: 1997-08-13
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2271 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-844-988-8

Query Match 100.0%; Score 90; DB 9; Length 2271;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 60
DB 1603 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 1662

QY 61 AAGCAGGGGGAACGCTGGACGACCTAGAG 90
DB 1663 AAGCAGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 8

US-10-338-462-8

Sequence 8, Application US/10338462

Publication No. US20030100026A1

GENERAL INFORMATION:

APPLICANT: Mercurio, Frank

Zhu, Hengyi

Barbosa, Miguel

Li, Gian

Murray, Brion W.

TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE

COMPLEX AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/338,462

APPLICATION NUMBER: US/10/338,462

FILING DATE: 08-Jan-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/844,908

FILING DATE: 27-Apr-2001

APPLICATION NUMBER: US/08/910,820

FILING DATE: 12-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 860098.413C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 2271 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-338-462-8

Query Match 100.0%; Score 90; DB 15; Length 2271;

Best Local Similarity 100.0%; Pred. No. 1.2e-21;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 60
DB 1603 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 1662

QY 61 AAGCAGGGGGAACGCTGGACGACCTAGAG 90
DB 1663 AAGCAGGGGGAACGCTGGACGACCTAGAG 1692

RESULT 9

US-09-796-872-14

Sequence 14, Application US/09796872

Patent No. US20020045235A1

GENERAL INFORMATION:

APPLICANT: Karin, Michael

APPLICANT: DiDonato, Joseph A.

APPLICANT: Rothwarf, David M.

APPLICANT: Hayakawa, Makio

APPLICANT: Zandi, Ebrahim

TITLE OF INVENTION: IKB Kinase, Subunits Thereof, and Methods of Using Same

FILE REFERENCE: P-UD 3295

CURRENT APPLICATION NUMBER: US/09/796,872

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 09/168,629

PRIOR FILING DATE: 1998-10-08

PRIOR APPLICATION NUMBER: 60/061,470

PRIOR FILING DATE: 1997-10-09

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14

LENGTH: 2931

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (36)..(2306)

US-09-796-872-14

Query Match 100.0%; Score 90; DB 9; Length 2931;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 60
DB 1638 GAACGGATGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGGCCGG 1697

QY 61 AAGCAGGGGGAACGCTGGACGACCTAGAG 90

DB 1698 AAGCAGGGGGAACGCTGGACGACCTAGAG 1727

RESULT 10

US-10-087-192-1757

Sequence 1757, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: CANCER

FILE REFERENCE: 529452000122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1757

LENGTH: 4154

TYPE: DNA

ORGANISM: Homo sapiens

US-10-087-192-1757

Query Match 100.0%; Score 90; DB 13; Length 4154;

```
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGG 60
Db 1813 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGG 1872

Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1873 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1902

RESULT 11
US-10-087-192-1756
; Sequence 1756, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1756
; LENGTH: 81099
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(81099)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1756

Query Match 95.6%; Score 86; DB 13; Length 81099;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGG 60
Db 59517 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGG 59576

Qy 61 AAGCAGGGGGGAACGCTGGACGACCT 86
Db 59577 AAGCAGGGGGGAACGCTGGACGACCT 59602

RESULT 12
US-10-156-610-83
; Sequence 83, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
; FILE REFERENCE: ISPH-0666
; CURRENT APPLICATION NUMBER: US/10/156,610
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/856,246
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US99/16959
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/197,008
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 83
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; LENGTH: 3038
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-156-610-83

Query Match 85.8%; Score 77.2; DB 15; Length 3038;
Best Local Similarity 91.1%; Pred. No. 3.5e-17;
Matches 82; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGG 60
Db 1628 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACCTACAGAGAGCCCATGGTGG 1687

Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1688 AAGCAGGGGGGACCTTGGATGACCTAGAG 1717

RESULT 13
US-10-156-610-48
; Sequence 48, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
; FILE REFERENCE: ISPH-0666
; CURRENT APPLICATION NUMBER: US/10/156,610
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/856,246
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US99/16959
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/197,008
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 48
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-156-610-48

Query Match 82.2%; Score 74; DB 15; Length 2274;
Best Local Similarity 88.9%; Pred. No. 4.6e-16;
Matches 80; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGAGCCCATGGCGG 60
Db 1603 GAGCGGATGATGGCACTGCAGACTGACATTGTGGACCTGCAGAGAGCCCATGGTGG 1662

Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
Db 1663 AAGCAGGGGGGACCTTGGATGACCTAGAG 1692

RESULT 14
US-10-087-192-1754
; Sequence 1754, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1754
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-1754

Query Match      82.2%; Score 74; DB 13; Length 3210;
Best Local Similarity 88.9%; Pred. No. 4.6e-16;
Matches 80; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GAACGGATGATGGCTCTGCAGACCGACATTTGGACTTACAGAGGAGCCCATGGGCCGG 60
   |||||||
Db 1647 GAGCGGATGATGCGCTGCGACTGACATTTGGACCTGCAGAGGAGCCCGATGGGTCGG 1706
   |||||||

QY 61 AAGCAGGGGGGGAACGCTGACGACCTAGAG 90
   |||||||
Db 1707 AAGCAGGGGGGACCCCTGGATGACCTAGAG 1736
   |||||||

RESULT 15
US-10-087-192-1753
; Sequence 1753, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1753
; LENGTH: 67076
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(67076)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1753

Query Match      77.8%; Score 70; DB 13; Length 67076;
Best Local Similarity 88.4%; Pred. No. 1.4e-14;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GAACGGATGATGGCTCTGCAGACCGACATTTGGACTTACAGAGGAGCCCATGGGCCGG 60
   |||||||
Db 48916 GAGCGGATGATGGCACTGCGACTGACATTTGGACCTGCAGAGGAGCCCGATGGGTCGG 48975
   |||||||

QY 61 AAGCAGGGGGGGAACGCTGACGACCT 86
   |||||||
Db 48976 AAGCAGGGGGGACCCCTGGATGACCT 49001
   |||||||

Search completed: September 24, 2004, 03:50:57
Job time : 383 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:54 ; Search time 121 Seconds
(without alignments)
70.053 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360

Perfect score: 151

Sequence: 1 ERMAQTQDIVDLQRSPMGKQGGTLLDLE 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	100.0	149	4 AAB63781	Aab63781 Human pro
2	151	100.0	552	3 AAY84883	Aay84883 A GFP-I-k
3	151	100.0	750	5 ABB77294	Abb77294 Human IKK
4	151	100.0	756	2 AAW56328	Aaw56328 Inhibitor
5	151	100.0	756	2 AAW49097	Aaw49097 Human I-k
6	151	100.0	756	2 AAW82499	Aaw82499 Human IKK
7	151	100.0	756	2 AAW96158	Aaw96158 Human I k
8	151	100.0	756	2 AAY43247	Aay43247 Human inh
9	151	100.0	756	2 AAW86163	Aaw86163 Human IKK
10	151	100.0	756	2 AAY24051	Aay24051 Human kin
11	151	100.0	756	2 AAW81566	Aaw81566 Ikb kinas
12	151	100.0	756	2 AAY14515	Aay14515 Human IKK
13	151	100.0	756	2 AAW81563	Aaw81563 Ikb kinas
14	151	100.0	756	5 ABB77306	Abb77306 Human IKK
15	151	100.0	756	5 ABB77296	Abb77296 Human IKK
16	151	100.0	756	5 ABB77295	Abb77295 Human IKK
17	151	100.0	756	5 ABB77300	Abb77300 Human IKK
18	151	100.0	756	5 ABB77293	Abb77293 Human IKK
19	151	100.0	756	5 ABB77304	Abb77304 Human IKK
20	151	100.0	756	5 ABB77298	Abb77298 Human IKK
21	151	100.0	756	5 ABB77302	Abb77302 Human IKK
22	151	100.0	756	5 ABB77297	Abb77297 Human IKK
23	151	100.0	756	5 ABB77308	Abb77308 Human IKK
24	151	100.0	756	5 ABB77307	Abb77307 Human IKK
25	151	100.0	756	5 ABB77299	Abb77299 Human IKK

ALIGNMENTS

RESULT 1

AAB63781
ID AAB63781 standard; protein; 149 AA.

XX AAB63781;

XX AC (first entry)

XX DT 26-MAR-2001

XX XX Human prostate cancer associated antigen protein sequence SEQ ID NO:1143.

XX DE Human; breast cancer; gastric cancer; prostate cancer; diagnosis;

XX KW cancer associated antigen; cytostatic; cancer vaccine.

XX OS Homo sapiens.

XX XX WO200073801-A2.

XX PN 07-DEC-2000.

XX PD 26-MAY-2000; 2000WO-US014749.

XX PP 28-MAY-1999; 99US-0136526P.

XX PR 10-SEP-1999; 99US-0153454P.

XX XX (LUDW-) LUDWIG INST CANCER RES.

XX PA Obata Y;

XX PI WPI; 2001-025274/03.

XX XX Nucleic acids encoding breast, gastric and prostate cancer associated

XX DR antigen precursors, useful for diagnosing and treating a condition

XX PT characterized by expression of an abnormal amount of a protein, e.g.

XX PT cancer.

XX PS Example 1; Page 715; 799pp; English.

XX XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014

XX CC represent nucleotide sequences encoding human breast, gastric and

XX CC prostate cancer associated antigen precursors (CAAP) respectively.

XX CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970

XX CC represent human breast, gastric and prostate CAAP protein sequence

XX CC respectively. CAAPs have cytostatic activity and can be used in the

XX CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic

XX CC acids or anti-CAAP antibodies are useful for diagnosing and treating a

XX CC condition characterised by expression of an abnormal amount of a protein,

XX CC e.g. cancer

XX XX

Abb77301 Human IKK
Abb77305 Human IKK
Abb77310 Human IKK
Abb77303 Human IKK
Abb77309 Human IKK
Abb775804 Human IKK
Abo32508 Human ini
Aay84882 Amino aci
Aay84880 Amino aci
Aay92057 Murine I
Abb57325 Mouse isc
Abr42682 Mouse IKK
Aaw56329 Inhibitor
Aaw82498 Human IKK
Aaw96157 Human IKK
Aaw86164 Human kin
Aay24052 Human kin
Aaw81565 Ikb kinas
Aay14516 Human IKK

SQ Sequence 149 AA;

Query Match 100.0%; Score 151; DB 4; Length 149;
 Best Local Similarity 100.0%; Pred. No. 5.7e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
 |||||
 DB 9 ERMALQTDIVDLQSPMGKQGGTLDLLE 38

RESULT 2
 AAY84883
 ID AAY84883 standard; protein; 552 AA.
 XX
 AC AAY84883;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE A GFP-I-kappaB kinase-LZ domain fusion protein.
 XX
 KW I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
 KW cyclic GMP; PDE3; PDE7; PDE8; PDE4 splice variant; PDE4D;
 KW inflammatory disease; chronic inflammation; airway disease; asthma;
 KW chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis;
 KW pellospondylitis; bowel disease; ulcerative colitis; Crohn's disease;
 KW autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis;
 KW systemic lupus erythematous; myasthenia gravis; Grave's disease;
 KW immune thrombocytopenic purpura; acute respiratory distress syndrome;
 KW septic shock; depression; PDE1; PDE2; PDE6; PDE9; PDE10; Jet lag;
 KW PDE5 splice variant; tension; erectile dysfunction; circadian rhythm;
 KW green fluorescent protein; GFP.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Aequorea victoria.
 XX
 PN WO200023091-A2.
 XX
 PD 27-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-DK000567.
 XX
 PR 15-OCT-1998; 98DK-00001321.
 PR 15-OCT-1998; 98DK-00001322.
 PR 15-OCT-1998; 98DK-00001323.
 XX
 PA (BIOI-) BIOIMAGE AS.
 XX
 PI Arkhammar POG, Terry BR, Scudder KM, Bjorn SP, Thastrup O;
 XX
 DR WPI; 2000-399281/34.
 DR N-PSDB; AAA14961.
 XX
 PT Modulating the activity of I-kappaB kinases or cyclic nucleotide
 phosphodiesterases for the treatment of inflammatory disorders,
 PT autoimmune disorders (e.g. diabetes and Crohn's disease) and depression.
 XX
 PS Example 3; Page 127-128; 128pp; English.
 XX
 CC The specification describes a method for modulating the specific
 effectiveness of I-kappaB kinases or cyclic nucleotide phosphodiesterases
 CC which have the ability to cleave cyclic AMP and/or GMP. This involves
 CC modulating the specific effectiveness of the cyclic nucleotide
 CC phosphodiesterase or I-kappaB kinase by modulating the spatial
 CC distribution within cells of the animal. If the cyclic nucleotide
 CC phosphodiesterase used is a PDE3, PDE7, PDE8 or a splice variant of PDE4
 CC (such as PDE4D), the method is used to treat inflammatory diseases such
 CC as chronic inflammation (especially airway diseases such as asthma and
 CC chronic bronchial hyper-reactivity of non-asthma etiology, joint
 CC disorders such as rheumatoid arthritis and pellospondylitis and bowel
 CC diseases such as ulcerative colitis and Crohn's disease), autoimmune
 CC diseases associated with inflammation (such as diabetes mellitus type I,

CC systemic lupus erythematous, myasthenia gravis, Hashimoto's
 CC thyroiditis, Grave's disease and immune thrombocytopenic purpura),
 CC dysregulations of the immune system (such as acute respiratory distress
 CC syndrome (ARDS) and septic shock) and/or depression. Alternatively, if
 CC the cyclic nucleotide phosphodiesterase is PDE1, PDE2, PDE6, PDE9, PDE10
 CC or a splice variant of PDE5, the method is used to treat hypo- or
 CC hypertension, erectile dysfunction, circadian rhythm resetting or jet-
 CC lag. The present sequence represents a fusion protein of green
 CC fluorescent protein (GFP) and I-kappaB kinase and the LZ domain, which is
 CC used in the course of the invention
 XX
 SQ Sequence 552 AA;

Query Match 100.0%; Score 151; DB 3; Length 552;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
 |||||
 DB 331 ERMALQTDIVDLQSPMGKQGGTLDLLE 360

RESULT 3
 ABB77294
 ID ABB77294 standard; protein; 750 AA.
 XX
 AC ABB77294;
 XX
 DT 14-JUN-2002 (first entry)
 XX
 DE Human IKKbeta mutant delNBN 737-742.
 XX
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteostatic; cytostatic; neutropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200183547-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US040654.
 XX
 PR 02-MAY-2000; 2000US-0201261P.
 PR 22-AUG-2000; 2000US-00643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain.
 XX
 PS Example 4; Page; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound (ABB08725-
 CC ABB08742) comprising at least one NEMO binding domain (ABB77313). The
 CC compound has acts through selective inhibition of cytokine-mediated NF-kB
 CC activation by blocking the interaction of NEMO with IKKbeta at the NEMO

CC binding domain. Blockage of IKKbeta-NEMO interaction results in
 CC inhibition of IKKbeta kinase activation and subsequent decreased
 CC phosphorylation of Ikbppab. The compound may also act (directly or
 CC indirectly) by blocking the recruitment of leukocytes into sites of acute
 CC and chronic inflammation, by down-regulating the expression of E-selectin
 CC on leukocytes or by blocking osteoclast differentiation. The compound is
 CC useful in treating NF-kB mediated conditions, where the condition is an
 CC inflammatory disorder, an autoimmune disease, transplant rejection,
 CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
 CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
 CC allergies, uveitis, anaphylaxis, cutaneous inflammation, sepsis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
 CC inflammatory bowel disease, chronic obstructive pulmonary disease,
 CC vasculitis and bursitis. The inflammatory disorder may also be
 CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
 CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC deletion mutant, useful in examples of the invention. Note: The present
 CC sequence is not given in the specification but is derived from GenBank
 CC Accession No. 014920 (ABB77294)

XX Sequence 750 AA;

Query Match 100.0%; Score 151; DB 5; Length 750;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGLDLE 30
 |||||
 Db 535 ERMALQTDIVDLQSPMGKQGGLDLE 564

RESULT 4

ID AAW56328 standard; protein; 756 AA.

XX AAW56328;

XX 24-JUL-1998 (first entry)

XX Inhibitory subunit I-kappa-B signalsome kinase 2 amino acid sequence.

XX Inhibitory subunit; I-kappa-B-beta; nuclear factor kappa-B;
 KW NF-kappa-B/Rel dimer; inhibitory activity; phosphorylation;
 KW stimulus-inducible I-kappa-B kinase; IKK; signalsome; I-kappa-B-alpha;
 KW identification; stimulate; signal transduction; the NF-kappa-B cascade;
 KW therapeutic composition; inflammatory; neurodegenerative; disease;
 KW autoimmune disease; cancer.

XX Homo sapiens.

XX WO9808955-A1.

XX 05-MAR-1998.

XX 26-AUG-1997; 97WO-US015003.

XX 26-AUG-1996; 96US-00697393.

XX 13-AUG-1997; 97US-00910820.

XX (SIGN-) SIGNAL PHARM INC.

XX Mercurio F, Zhu H, Barbosa M, Li G, Murray BW;

XX WPI; 1998-179440/16.
 DR N-ESDB; AAV22842.

XX New isolated stimulus-inducible I-kappa-B kinase signalsome - useful for
 PT developing products for treating, e.g. inflammatory neuro-degenerative
 PT and auto-immune diseases.

XX Claim 3; Page 60-64; 115pp; English.

XX The present sequence represents an inhibitory subunit I-kappa-B kinase
 CC (IKK) 2. IKK kinases, when incorporated into an IKK signalsome, are
 CC capable of phosphorylating inhibitory subunit I-kappa-B-alpha, at serine
 CC residues 32 and 36. I-kappa-B-alpha retains nuclear factor (NF) kappa-B
 CC in the cytoplasm. I-kappa-B proteins contain 5-7 ankyrin-like repeats
 CC which are required for association with the NF-kappa-B/Rel dimer and for
 CC inhibitory activity. A stimulus-inducible IKK "signalsome" is described
 CC that is capable of specifically phosphorylating I-kappa-B-alpha at
 CC residues S32 and S36, without the addition of exogenous cofactors. The
 CC proteins of the invention can be used to identify agents that inhibit or
 CC stimulate signal transduction via the NF-kappa-B cascade. Therapeutic
 CC compositions comprising such agents may be used for treating a patient
 CC afflicted with a disorder associated with the activation of an IKK
 CC signalsome. The agents may be used to treat, e.g. inflammatory,
 CC neurodegenerative diseases and autoimmune diseases, cancer and viral
 CC infections. The antibodies may be used in a kit for detecting IKK
 CC signalsome activity in a sample

XX Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;

Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGLDLE 30
 |||||
 Db 535 ERMALQTDIVDLQSPMGKQGGLDLE 564

RESULT 5

AAW49097

ID AAW49097 standard; protein; 756 AA.

XX AAW49097;

XX 07-DEC-1998 (first entry)

XX Human I-kappa-B kinase (IKK) beta subunit.

XX I-kappa-B kinase; IKK; human; protein kinase; NF-kappa-B; inflammation;
 KW signal transduction.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 15..300

XX Region /note= "kinase domain"

XX /note= "regions contains leucine residues involved in

XX leucine zippers"

XX Domain 602..642

XX /note= "helix-loop-helix domain"

XX WO9837228-A1.

XX 27-AUG-1998.

XX 23-FEB-1998; 98WO-US003511.

XX 25-FEB-1997; 97US-00810131.

XX 09-OCT-1997; 97US-0061470P.

XX (REGC) UNIV CALIFORNIA.

XX Karin M, Didonato JA, Rothwarf DM, Hayakawa M, Zandi E;
 PI WPI; 1998-467580/40.
 XX DR N-PSDB; AAV32970.
 XX Nucleic acid encoding I-kappa-B kinase subunits and antibodies - the sub-
 PT units phosphorylate the inhibitor of NF-kappa-B, for studying the
 PT inflammatory response and signal transduction pathways.
 XX Claim 3; Fig 3; 101pp; English.
 XX This is the amino acid sequence of the alpha beta of a human serine
 CC protein kinase, designated I-kappa-B kinase (IKK). The IKK beta and alpha
 CC (see AAW49096) subunits are cytokine-inducible, share substantial
 CC sequence homology, and are activated in response to proinflammatory
 CC signals to phosphorylate proteins (I-kappa-Bs) that inhibit the activity
 CC of the NF-kappa-B transcription factor. Their amino acid sequences were
 CC deduced from cDNA clones (see AAV32969-70). The invention also provides
 CC vectors comprising IKK-alpha and -beta nucleic acid molecules, isolated
 CC IKK catalytic subunits which can phosphorylate the I-kappa-B protein at
 CC Ser-32 and Ser-36, and peptide portions of such IKK subunits. The
 CC invention also provides anti-IKK antibodies and their IKK-binding
 CC fragments, as well as methods of purifying an IKK complex, methods of
 CC identifying an agent which alters the association of an IKK complex or an
 CC IKK catalytic subunit with a second protein, and methods of identifying
 CC proteins that can interact with an IKK complex or an IKK catalytic
 CC subunit. IKK nucleic acids, catalytic subunits and antibodies may be used
 CC to study the signal transduction pathways involved in the inflammatory
 CC and immune responses, and to identify agents that alter IKK activity,
 CC such as protein kinase inhibitors
 XX Sequence 756 AA;
 SQ

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDDLE 30
 |||||
 Db 535 ERMALQTDIVDLQSPMGKKGGLDDLE 564

RESULT 6
 AAW82499
 ID AAW82499 standard; protein; 756 AA.
 XX AC AAW82499;
 XX 04-MAR-1999 (first entry)
 XX Human IKK-beta protein.
 XX NIK; Nuclear factor-kappa B; NF-kB; signal transduction; TNF; human;
 KW tumour necrosis factor; NF-kB-inducing kinase; screening; interaction;
 KW modulator; immune response; inflammatory response; viral gene;
 KW diagnostic; therapy; IKK-beta.
 XX Homo sapiens.
 OS US5854003-A.
 PN 29-DEC-1998.
 XX 26-FEB-1998; 98US-00032475.
 XX 03-JUL-1997; 97US-00087518.
 XX (TULA-) TULARIK INC.
 XX Wu L, Rothe M;
 PI WPI; 1999-094902/08.

XX Screening agents for modulating interaction of nuclear factor kappaB
 PT inducing kinase - with kinase-binding target, useful for controlling
 PT levels of the kinase, for treatment and diagnosis of conditions
 PT associated with e.g. inhibition of signal transduction by tumour necrosis
 PT factor.
 XX Disclosure; Col 23-28; 16pp; English.
 XX This sequence represents the human IKK-beta protein, which is used in the
 CC isolation of a novel nuclear factor-kappaB (NFkB)-inducing kinase (NIK).
 CC This protein is used to screen for agents that modulate the interaction
 CC of NIK with a NIK-binding target. The protein can be used as a modulator
 CC of cellular functions at the NIK level, or for development of such
 CC compounds. NFkB is involved in expression of many immune and inflammatory
 CC responses and of some important viral genes. The protein may be used
 CC diagnostically and therapeutically, in conditions associated with
 CC abnormal utilisation of pathways that involve NFkB, e.g. inhibition of
 CC signal transduction by tumour necrosis factor (TNF)
 XX Sequence 756 AA;
 SQ

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDDLE 30
 |||||
 Db 535 ERMALQTDIVDLQSPMGKKGGLDDLE 564

RESULT 7
 AAW96158
 ID AAW96158 standard; peptide; 756 AA.
 XX AC AAW96158;
 XX 27-APR-1999 (first entry)
 XX Human I kappa B kinase.
 XX I-kappa-B kinase; IKK-alpha; gene expression; modulation; suppression;
 KW activation; tumour necrosis factor; TNF; interleukin-1; IL-1;
 KW TNF receptor associated factor; TRAF.
 XX Homo sapiens.
 OS WO9901541-A1.
 PN 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US013782.
 XX 01-JUL-1997; 97US-00087115.
 XX 10-JUL-1997; 97US-00090854.
 XX (TULA-) TULARIK INC.
 XX Rothe M, Cao Z, Regnier C;
 PI WPI; 1999-106044/09.
 XX N-PSDB; AAX08919.
 XX Newly isolated human kinase IkappaB Kinase (IKK- α) polypeptides - useful
 PT in screening for agents that modulate the interaction of an IKK
 PT polypeptide to a binding target and for modulating signal transduction
 PT involving IkappaB in a cell.
 XX Claim 9; Page 21-23; 32pp; English.
 XX I-kappa-B, deletion mutants of it retaining I-kappa-B kinase activity and
 CC I-kappa-B polypeptides (comprising a six residue domain of I-kappa-B
 CC containing one of Ser32 and Ser36, and a candidate agent) can be used to

CC screen for agents that modulate the interaction of an IKK polypeptide to
 CC a binding target. The modulation of the kinase activity of IKK-alpha
 CC (AAW96157) forms a method for modulating signal transduction involving I-
 CC kappa-B in a cell. The IKK-alpha polypeptides are useful for generating
 CC oligonucleotide primers and probes for use in the isolation of natural
 CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
 CC translatable transcripts, hybridization probes, polymerase chain reaction
 CC (PCR) probes and primers. Their diagnostic applications include IKK-alpha
 CC hybridization probes for identifying wild-type and mutant IKK-alpha
 CC alleles in clinical and laboratory samples. Therapeutic application
 CC includes the use of IKK- alpha nucleic acids for modulating cellular
 CC expression or intracellular concentration/availability of active IKK-
 CC alpha. Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
 CC activation induced by tissue necrosis factor (TNF), interleukin-1 (IL-1)
 CC stimulation, TNF receptor-associated factor (TRAF), and NF-kappa-B-
 CC inducing Kinase (NIK) overexpression
 CC
 XX SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ERMMALQTDIVDLQSPMGKQGGTLDLLE 30
 |||||
 Db 535 ERMMALQTDIVDLQSPMGKQGGTLDLLE 564

RESULT 8
 AAY43247
 ID AAY43247 standard; protein; 756 AA.
 XX
 AC AAY43247;
 XX
 DT 13-JAN-2000 (first entry)
 XX
 DE Human inhibitor-kappa B kinase-beta protein sequence.

XX Inhibitor-kappa B kinase-beta; IKB-beta; human; T-cell leukaemia; asthma;
 KW inflammatory response; inflammatory disease; juvenile diabetes mellitus;
 KW Graves' disease; rheumatoid arthritis; allograft rejection; diagnosis;
 KW inflammatory bowel disease; multiple sclerosis; contact dermatitis;
 KW rhinitis; allergy; hyperproliferative disorder; tumour; therapy.

XX Homo sapiens.
 XX US977341-A.
 XX
 XX 02-NOV-1999.
 XX
 XX 20-NOV-1998; 98US-00197008.
 XX
 XX 20-NOV-1998; 98US-00197008.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Cowser LM;
 XX
 XX WPI; 1999-619715/53.
 XX N-PSDB; AAZ31590.

PT Antisense oligonucleotides inhibiting human Inhibitor-kappa B Kinase-
 PT beta, useful for treating conditions such as inflammation, asthma,
 PT diabetes, allograft rejection, allergies, hyperproliferative disorders or
 PT tumors.

XX Claim 1; Col 41-48; 32pp; English.
 XX
 CC This sequence represents the human inhibitor-kappa B kinase-beta. The
 CC invention relates to an antisense oligonucleotide (I) 8 to 30 nucleotides
 CC in length inhibiting the expression of human Inhibitor-kappa B kinase-
 CC beta (IKB-beta). (I) inhibits the expression of human IKB-beta which
 CC plays a role in the development of T-cell leukaemia and in the activation

CC of inflammatory responses. (I) is therefore useful for treating
 CC inflammatory diseases or disorders with an inflammatory component such as
 CC asthma, juvenile diabetes mellitus, Graves' disease, rheumatoid
 CC arthritis, allograft rejection, inflammatory bowel disease, multiple
 CC sclerosis, contact dermatitis, rhinitis and various allergies, or
 CC hyperproliferative disorders such as leukaemias and other tumours. (I)
 CC may also be used for detection of the above disorders
 XX SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ERMMALQTDIVDLQSPMGKQGGTLDLLE 30
 |||||
 Db 535 ERMMALQTDIVDLQSPMGKQGGTLDLLE 564

RESULT 9
 AAW86163
 ID AAW86163 standard; protein; 756 AA.
 XX
 AC AAW86163;
 XX
 DT 03-MAR-1999 (first entry)
 XX
 DE Human IKK-beta polypeptide.

XX IKK-beta; IkappaB kinase; inhibitor; NF-kappaB; nuclear factor-kappaB;
 KW nuclear translocation; NF-kappaB-inducing Kinase; NIK; recombinant;
 KW human.

XX Homo sapiens.
 XX US5851812-A.
 XX
 XX 22-DEC-1998.

XX 10-JUL-1997; 97US-00890853.
 XX
 XX 01-JUL-1997; 97US-00887114.
 XX
 XX (TULA-) TULARIK INC.

XX Woronicz J, Goeddel DV;
 XX WPI; 1999-080407/07.
 XX N-PSDB; AAV84689.

XX DNA encoding IKK-beta polypeptides - useful for producing recombinant
 XX polypeptides.

XX Claim 8; Col 13-18; 13pp; English.

XX This represents a IKK-beta (IkappaB kinase) polypeptide. The IkappaB
 CC (inhibitor of nuclear factor (NF)-kappaB nuclear translocation) kinase is
 CC a NF-kappaB-inducing Kinase (NIK)-interacting protein. A host cell
 CC containing a recombinant nucleic acid encoding the IKK-beta polypeptide
 CC can be used for the recombinant production of the polypeptide
 XX

XX SQ Sequence 756 AA;
 Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ERMMALQTDIVDLQSPMGKQGGTLDLLE 30
 |||||
 Db 535 ERMMALQTDIVDLQSPMGKQGGTLDLLE 564

RESULT 10

```
AAAY24051
ID AAY24051 standard; protein; 756 AA.
XX
AC AAY24051;
XX
XX 20-MAR-2003 (revised)
DT 01-OCT-1999 (first entry)
XX
XX Human kinase I-kappa-B kinase (IKK-beta).
DE
XX Nuclear factor kappa-B inducing kinase; NIK; NIK-interacting protein;
KW human; I-kappa-B kinase; IKK-beta; IKK-beta disorder.
XX
XX Homo sapiens.
OS
XX US5939302-A.
PN
XX 17-AUG-1999.
PD
XX 17-JUN-1998; 98US-00099124.
PF
XX 01-JUL-1997; 97US-00887114.
PR
XX 10-JUL-1997; 97US-00890853.
XX
XX (TULA-) TULARIK INC.
PA
XX Woronicz J, Goeddel DV;
PI
XX WPI; 1999-468406/39.
DR
XX N-PSDB; AAX98271.
DR
XX Polypeptides comprising a novel I-kappa-B Kinase useful as hybridization
PT probes.
PT
XX Claim 2; Col 13-18; 13pp; English.
PS
XX The present sequence represents a human I-kappa-B kinase (IKK-beta). The
CC protein is a nuclear factor kappa-B inducing kinase (NIK) interacting
CC protein. The IKK-beta nucleic acids, polypeptides, and/or antibodies may
CC be useful as hybridization primers or probes, translatable transcripts,
CC diagnostic probes (e.g. for identifying the presence of IKK-beta in a
CC sample), to detect mutant IKK-beta alleles, in the diagnosis and therapy
CC of IKK-beta disorders, and in the identification of compounds or agents
CC that are able to modulate IKK-beta function. (Updated on 20-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 756 AA;
SQ
Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERMALQTDIVDLQSPMGKQGGTLDDLE 30
DB 535 ERMALQTDIVDLQSPMGKQGGTLDDLE 564
RESULT 11
AAW81566
ID AAW81566 standard; protein; 756 AA.
XX
XX AAW81566;
AC
XX 04-FEB-1999 (first entry)
DT
XX Ikb kinase (IKK)-beta polypeptide.
DE
XX NIK; Ikb; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition;
KW tumour necrosis factor; binding; genetic hybridisation; screening;
KW signal transduction; biopharmaceutical; human.
XX
XX Homo sapiens.
OS
XX
```

```
PN US5843721-A.
XX
PD 01-DEC-1998.
XX
XX 03-JUL-1997; 97US-00887518.
PF
XX 03-JUL-1997; 97US-00887518.
PR
XX (TULA-) TULARIK INC.
PA
XX Wu L, Rothe M;
PI
XX WPI; 1999-044580/04.
DR
XX
XX Probe, vector or recombinant nucleic acid encoding a polypeptide, - useful
PT especially human nuclear factor kappa-B-inducing kinase protein - useful
PT for producing recombinant protein.
PT
XX Example; Col 23-26; 15pp; English.
PS
XX This represents a Ikb kinase (IKK)-alpha polypeptide sequence. The
CC binding activity of this polypeptide can be activated or inhibited by the
CC nuclear factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide of the
CC invention. The NIK polypeptide or its fragment has one or more activities
CC selected from kinase activity and inhibitory activity; Ikb kinase-alpha
CC and beta binding activity and binding inhibitory activity; tumour
CC necrosis factor (TNF) receptor-associated factor 2 binding activity and
CC binding inhibitory activity; Ikb binding activity and binding inhibitory
CC activity, NF-kB activating and inhibitory activity. A vector containing
CC the NIK nucleic acid can be used to transform host cells for the
CC recombinant production of the protein. The NIK nucleic acid and the
CC polypeptide may be used in diagnosis (e.g. genetic hybridisation screen
CC for NIK transcripts), therapy (e.g. NIK kinase inhibitors to inhibit TNF
CC signal transduction), and in the biopharmaceutical industry
XX
XX Sequence 756 AA;
SQ
Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERMALQTDIVDLQSPMGKQGGTLDDLE 30
DB 535 ERMALQTDIVDLQSPMGKQGGTLDDLE 564
RESULT 12
AAV14515
ID AAV14515 standard; protein; 756 AA.
XX
XX AAV14515;
AC
XX 31-AUG-1999 (first entry)
DT
XX Human IKK-beta protein sequence.
DE
XX Human; IKK-beta; I-Kappa B-Kinase; inhibitory protein; diagnosis; NF-kB;
KW Nuclear Factor Kappa B; interaction; binding target.
XX
XX Homo sapiens.
OS
XX US5916760-A.
PN
XX 29-JUN-1999.
PD
XX 17-JUN-1998; 98US-00099125.
PF
XX 01-JUL-1997; 97US-00887114.
PR
XX 10-JUL-1997; 97US-00890853.
XX
XX (TULA-) TULARIK INC.
PA
XX Goeddel DV, Woronicz J;
PI
```

XX WPI; 1999-384722/32.
 DR N-PSDB; AAX79304.
 XX
 PT Screening for agents which modulate the interaction of IKK-beta
 PT polypeptides and their binding targets.
 XX
 PS Claim 2; Col 13-18; 14pp; English.
 XX
 CC This sequence represents human IKK-beta, a novel IKK Kinase (I-Kappa B-
 CC Kinase, one of a family of inhibitory proteins which interact with
 CC Nuclear Factor Kappa B (NF-kB)). The invention relates to a method of
 CC screening for agents which modulate the interaction of human IKK-beta
 CC polypeptides and their binding targets. Agents which modulate the IKK-
 CC beta binding are useful in a variety of diagnostic and therapeutic
 CC applications where the disease is associated with improper utilization of
 CC a pathway involving IKK-beta proteins (e.g. NF-kB activation and IKK-beta
 CC -dependent transcriptional activation)
 XX
 SQ Sequence 756 AA;
 Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERMALQTDIVDLQSPMGKQGGLDDLE 30
 DB 535 ERMALQTDIVDLQSPMGKQGGLDDLE 564
 RESULT 13
 AAW81563
 ID AAW81563 standard; protein; 756 AA.
 XX
 AC AAW81563;
 XX
 DT 04-FEB-1999 (first entry)
 XX
 DE IKK kinase (IKK)-beta polypeptide.
 XX
 KW NIK; IKK; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition;
 KW tumour necrosis factor; binding; genetic hybridisation; screening;
 KW signal transduction; biopharmaceutical; immunogen; pharmacological;
 KW transcription regulator; human.
 XX
 OS Homo sapiens.
 XX
 FN US5844073-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 13-FEB-1998; 98US-00023321.
 XX
 PR 03-JUL-1997; 97US-00887518.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Wu L, Rothe M;
 XX
 DR WPI; 1999-044664/04.
 XX
 XX New isolated peptide comprising a specified 947 amino acid sequence - has
 PT e.g. kinase activity, kinase inhibitory activity, IKK kinase-alpha
 PT binding activity, and IKK kinase-alpha binding inhibitory activity.
 XX
 PS Example; Col 23-26; 15pp; English.
 XX
 CC This represents a IKK kinase (IKK)-beta polypeptide sequence. The binding
 CC activity of this polypeptide can be activated or inhibited by the nuclear
 CC factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide of the
 CC invention. The NIK polypeptide or its fragment has one or more activities
 CC selected from kinase activity and inhibitory activity; IKK kinase-alpha
 CC and beta binding activity and binding inhibitory activity; tumour

CC necrosis factor (TNF) receptor-associated factor 2 binding activity and
 CC binding inhibitory activity; IKK binding activity and binding inhibitory
 CC activity, NF-kB activating and inhibitory activity. The NIK nucleic acid
 CC and the polypeptide may be used in diagnosis (e.g. genetic hybridisation
 CC screen for NIK transcripts), therapy (e.g. NIK kinase inhibitors to
 CC inhibit TNF signal transduction), and in the biopharmaceutical industry
 CC (e.g. as immunogens, reagents for isolating other transcription
 CC regulators, and reagents for screening chemical libraries for
 CC pharmacological agents)
 XX
 SQ Sequence 756 AA;
 Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERMALQTDIVDLQSPMGKQGGLDDLE 30
 DB 535 ERMALQTDIVDLQSPMGKQGGLDDLE 564
 RESULT 14
 ABB77306
 ID ABB77306 standard; protein; 756 AA.
 XX
 AC ABB77306;
 XX
 DT 14-JUN-2002 (first entry)
 XX
 DE Human IKKbeta mutant S740A.
 XX
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nontropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antiparasitic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 740 /note= "Wildtype Ser substituted by Ala"
 FT
 XX
 PN WO200183547-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US040654.
 XX
 PR 02-MAY-2000; 2000US-0201261P.
 PR 22-AUG-2000; 2000US-00643260.
 XX
 PA (UYUA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain.
 XX
 PS Example 11; Page; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound (ABB08725-

CC ABB08742) comprising at least one NEMO binding domain (ABB77313). The
 CC compound has acts through selective inhibition of cytokine-mediated NF-kB
 CC activation by blocking the interaction of NEMO with IKKbeta at the NEMO
 CC binding domain. Blockage of IKKbeta-NEMO interaction results in
 CC inhibition of IKKbeta kinase activation and subsequent decreased
 CC phosphorylation of IkappaB. The compound may also act directly or
 CC indirectly by blocking the recruitment of leukocytes into sites of acute
 CC and chronic inflammation, by down-regulating the expression of E-selectin
 CC on leukocytes or by blocking osteoclast differentiation. The compound is
 CC useful in treating NF-kB mediated conditions, where the condition is an
 CC inflammatory disorder, an autoimmune disease, transplant rejection,
 CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
 CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
 CC allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
 CC inflammatory bowel disease, chronic obstructive pulmonary disease,
 CC vasculitis and bursitis. The inflammatory disorder may also be
 CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
 CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections as
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention. Note: The present sequence
 CC is not given in the specification but is derived from Genbank Accession
 CC No. O14920 (ABB77294)

XX Sequence 756 AA;

Query Match 100.0%; Score 151; DB 5; Length 756;

Best Local Similarity 100.0%; Pred. No. 3.5e-14;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMMALQTDIVDLQSRPMGRKQGGLDLE 30

DB 535 ERMMALQTDIVDLQSRPMGRKQGGLDLE 564

RESULT 15

ABB77296

ID ABB77296 standard; protein; 756 AA.

AC ABB77296;

XX 14-JUN-2002 (first entry)

DE Human IKKbeta mutant W739P.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; muten.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 739

FT /note= "Wildtype Trp substituted by Phe"

XX

PN WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US040654.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (UYUA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.

XX inflammatory disorders, osteoporosis and cancer, comprises contacting a

XX cell with an anti-inflammatory compound comprising at least one NEMO

XX binding domain.

XX Example 11; Page; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell

XX comprises contacting a cell with an anti-inflammatory compound (ABB08725-

XX ABB08742) comprising at least one NEMO binding domain (ABB77313). The

XX compound has acts through selective inhibition of cytokine-mediated NF-kB

XX activation by blocking the interaction of NEMO with IKKbeta at the NEMO

XX binding domain. Blockage of IKKbeta-NEMO interaction results in

XX inhibition of IKKbeta kinase activation and subsequent decreased

XX phosphorylation of IkappaB. The compound may also act (directly or

XX indirectly) by blocking the recruitment of leukocytes into sites of acute

XX and chronic inflammation, by down-regulating the expression of E-selectin

XX on leukocytes or by blocking osteoclast differentiation. The compound is

XX useful in treating NF-kB mediated conditions, where the condition is an

XX inflammatory disorder, an autoimmune disease, transplant rejection,

XX osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral

XX infection or ataxia telangiectasia. The inflammatory disorder is asthma,

XX allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,

XX psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,

XX inflammatory bowel disease, chronic obstructive pulmonary disease,

XX vasculitis and bursitis. The inflammatory disorder may also be

XX dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus

XX and spondylarthritis. Also for Crohn's disease, ulcerative colitis,

XX polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,

XX cryoglobulinaemia or multiple sclerosis. For chronic viral infections

XX caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral

XX diseases include HIV and influenza. The compound may also be useful for

XX treating anaphylaxis, drug and food sensitivity, contact dermatitis,

XX sunburn or aging. The compound may be used to replace corticosteroids in

XX any application in which corticosteroids are used, including

XX immunosuppression in transplants and cancer therapy. Also for identifying

XX anti-inflammatory compounds and for diagnosis of an inflammatory disorder.

XX The compound may be administered alone or in combination with other known

XX anti-inflammatory agents. The present sequence is that of an IKKbeta

XX mutant, useful in examples of the invention. Note: The present sequence

XX is not given in the specification but is derived from Genbank Accession

XX No. O14920 (ABB77294)

XX Sequence 756 AA;

Query Match 100.0%; Score 151; DB 5; Length 756;

Best Local Similarity 100.0%; Pred. No. 3.5e-14;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMMALQTDIVDLQSRPMGRKQGGLDLE 30

DB 535 ERMMALQTDIVDLQSRPMGRKQGGLDLE 564

Search completed: September 24, 2004, 09:43:05

Job time : 123 secs

A>Note: the E. coli enzyme is the beta chain of the fatty acid complex
C:Superfamily: acetyl-CoA acetyltransferase
C:Keywords: acyltransferase; coenzyme A; fatty acid beta-oxidation
F:91/Active site: Cys #status predicted

Query Match	35.8%	Score 54;	DB 1;	Length 387;
Best Local Similarity	61.1%;	Pred. No. 2.4;	Mismatches 5;	Indels 0;
Gaps	0;			

Qy 7 QTDIVDLQRSPMGKRGKG 24
| | | | | : | | | | |
Db 3 QVIVDAIRTPMGRSKGG 20
| | | | | : | | | | |

RESULT 4
E91225
acetyl-CoA transferase [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: E91225
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91225
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <HAY>
A:Cross-references: GB:BAO00007; PIDN:BAB38196.1; PID:g13364249; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs4773
C:Superfamily: acetyl-CoA acetyltransferase

Query Match	35.8%	Score 54;	DB 2;	Length 387;
Best Local Similarity	61.1%;	Pred. No. 2.4;	Mismatches 5;	Indels 0;
Gaps	0;			

Qy 7 QTDIVDLQRSPMGKRGKG 24
| | | | | : | | | | |
Db 3 QVIVDAIRTPMGRSKGG 20
| | | | | : | | | | |

RESULT 5
C86072
acetyl-CoA transferase [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C:Accession: C86072
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.S.;
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.;
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C86072
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <STO>
A:Cross-references: GB:AE005174; MID:g12518723; PIDN:AAG59039.1; GSPDB:GN00145
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: fadA
C:Superfamily: acetyl-CoA acetyltransferase

Query Match	35.8%	Score 54;	DB 2;	Length 387;
Best Local Similarity	61.1%;	Pred. No. 2.4;	Mismatches 5;	Indels 0;
Gaps	0;			

Qy 7 QTDIVDLQRSPMGKRGKG 24
| | | | | : | | | | |
Db 3 QVIVDAIRTPMGRSKGG 20
| | | | | : | | | | |

```

RESULT 6
AI0914
small (beta) chain of the fatty acid-oxidizing multienzyme complex [imported] - Salmonella
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AI0914
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AI0914
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07911.1; PID:g16504456; GSPDB:GN00176
C:Genetics:
A:Gene: STY3578
C:Superfamily: acetyl-CoA acetyltransferase

Query Match 35.8%; Score 54; DB 2; Length 387;
Best Local Similarity 61.1%; Pred. No. 2.4;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 QTDIVDLQRSPMGRKQGG 24
||| ||| ||| |||
Db 3 QVIVDAIRTPMGRSKGG 20

RESULT 7
JS0624
fatty-acid beta-oxidation multienzyme complex beta chain - Pseudomonas fragi
N:Alternate names: acetyl-CoA C-acyltransferase homolog
N:Contains: acetyl-CoA C-acyltransferase (EC 2.3.1.16)
C:Species: Pseudomonas fragi
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JS0624; PS0268
R:Sato, S.; Hayashi, M.; Imamura, S.; Ozeki, Y.; Kawaguchi, A.
J. Biochem. 111, 8-15, 1992
A>Title: Primary structures of the genes, faoA and faoB, from Pseudomonas fragi B-0771 w
A:Reference number: JX0199; MUID:92299657; PMID:1607366
A:Accession: JS0624
A:Molecule type: DNA
A:Residues: 1-391 <SAT>
A:Cross-references: GB:D10390; GB:D90447; NID:g391838; PIDN:BAA01228.1; PID:g391840
A:Experimental source: strain B-0771
A:Accession: PS0268
A:Molecule type: protein
A:Residues: 20-41;161-182;207-229;262-294;298-320;336-350,'X',352-353 <SAT1>
C:Genetics:
A:Gene: faoB
C:Function: heterotetramer of 2 alpha and 2 beta chains
A:Description: catalyzes the cleavage of a 3-ketoacyl-coenzyme A by coenzyme A to acetyl
A:Pathway: fatty acid beta-oxidation
C:Superfamily: acetyl-CoA acetyltransferase
C:Keywords: acyltransferase; coenzyme A; fatty acid beta-oxidation; heterotetramer
F:2-391/Product: fatty-acid beta-oxidation multienzyme complex beta chain #status predic

Query Match 35.8%; Score 54; DB 1; Length 391;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 IVDLQRSPMGRKQGG 24
||| ||| ||| |||
Db 10 IVDGRTPMGRSKGG 24

RESULT 8
JS0624
fatty-acid beta-oxidation multienzyme complex beta chain - Pseudomonas aeruginosa (str
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83269
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, L.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: F83269
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <SPT>
A:Cross-references: GB:AE004726; GB:AE004091; NID:g9949108; PIDN:AAG06401.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: faoB; PA3013
C:Superfamily: acetyl-CoA acetyltransferase

Query Match 35.8%; Score 54; DB 2; Length 391;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 IVDLQRSPMGRKQGG 24
||| ||| ||| |||
Db 10 IVDGRTPMGRSKGG 24

RESULT 9
A82036
fatty oxidation complex, beta chain VC2759 [imported] - Vibrio cholerae (strain N16961 se
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <HEI>
A:Cross-references: GB:AE004342; GB:AE003852; NID:g9657358; PIDN:AAF95898.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2759
A:Map position: 1
C:Superfamily: acetyl-CoA acetyltransferase

Query Match 35.1%; Score 53; DB 2; Length 387;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 IVDLQRSPMGRKQGG 24
||| ||| ||| |||
Db 6 IVDLRTPMGRSKGG 20

RESULT 10
C90113
glucose inhibited division protein A [imported] - Giardia theta nucleomorph
C:Species: nucleomorph Giardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C:Accession: C90113
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A>Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
```

A;Accession: C90113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-649 <DOU>
A;Cross-references: GB:AJ010592; NID:gl2580753; PIDN:CAC27071.1; GSPDB:GN00151
C;Genetics:
A;Gene: putative N-terminal transit sequence
A;Map position: 2
A;Genome: nucleomorph
C;Superfamily: gida protein
C;Keywords: nucleomorph

Query Match 34.8%; Score 52.5; DB 2; Length 649;
Best Local Similarity 41.4%; Pred. No. 7.1;
Matches 12; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDL 29
Db 459 EYRMLLRGDNADIRLKLGRKY-GLVDDI 486

RESULT 11
AG0458
acetyl-CoA C-acyltransferase (EC 2.3.1.16) [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG0458
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG0458
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93235.1; PID:g15981682; GSPDB:GN00175
C;Genetics:
A;Gene: fadA
C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A

Query Match 34.4%; Score 52; DB 2; Length 387;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 IVDLQSPMGKQGG 24
Db 6 IIDAVRTPMGSKGG 20

RESULT 12
JQ0729
60K inner-membrane protein - Proteus mirabilis (fragment)
C;Species: Proteus mirabilis
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C;Accession: JQ0729
R;Skovgaard, O.
Gene 93, 27-34, 1990
A;Title: Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to the 60K-
A;Reference number: JQ0729; MUID:91033012; PMID:2172087
A;Accession: JQ0729
A;Molecule type: DNA
A;Residues: 1-237 <SKO>
A;Cross-references: GB:M56352; GB:M31295; NID:g150873; PIDN:AAA83954.1; PID:g150874
A;Experimental source: strain LM1509
C;Keywords: DNA replication; membrane protein

Query Match 33.8%; Score 51; DB 2; Length 237;
Best Local Similarity 31.0%; Pred. No. 4;
Matches 9; Conservative 12; Mismatches 4; Indels 4; Gaps 1;

QY 2 RMALQTDIVDLQSPMGKQGGTLDL 30
Db 61 KLITVTDVLDLRIN----TGGTIDEAD 85

RESULT 13
C83776
oxidoreductase BH1011 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C83776
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira-
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83776
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:gl0173440; PIDN:BA04730.1; GSPDB:GN000000000
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1011
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 32.8%; Score 49.5; DB 2; Length 297;
Best Local Similarity 39.3%; Pred. No. 8.7;
Matches 11; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 1 ERMALQTDIVDLQSPMGKQGGTIDD 28
Db 103 DSLRLQTDYIDLY-----QLHGGTIDD 125

RESULT 14
E86530
initiation factor-2 [imported] - Chlamydomophila pneumoniae (strain J138)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E86530
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-890 <STO>
A;Cross-references: GB:BA000008; NID:g8978691; PIDN:BAA98527.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo

Query Match 32.5%; Score 49; DB 2; Length 890;
Best Local Similarity 38.1%; Pred. No. 34;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 3 MMALQTDIVDLQSPMGKQGG 23
Db 553 MLALQAEVLELKADFSARAG 573

RESULT 15
E81576
translation initiation factor 2 CP0440 [imported] - Chlamydomophila pneumoniae (strain AR3)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
C;Accession: E81576
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, P.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-890 <REA>
A;Cross-references: GB:AE002205; GB:AE002161; NID:g7189360; PIDN:AAF38279.1; PID:g718936
A;Experimental source: strain AE39, HL cells
C;Genetics:
A;Gene: CP0440
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom
Query Match 32.5%; Score 49; DB 2; Length 890;
Best Local Similarity 38.1%; Pred. No. 34;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 3 MMALQTDIVDLQSPMGKQG 23
|:|:| :|:| :|:|
Db 553 MLALQAEVLELKADPSARAG 573

Search completed: September 24, 2004, 09:46:21
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:54 ; Search time 23 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERWALQTDIVDLQSPMKRGQGTLDLLE 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	100.0	756	1	IKKB HUMAN
2	151	100.0	757	1	IKKB MOUSE
3	151	100.0	757	1	IKKB RAT
4	84	55.6	745	1	IKKA MOUSE
5	79	52.3	745	1	IKKA HUMAN
6	54	35.8	387	1	THIK_ECO57
7	54	35.8	387	1	THIK_ECOLI
8	54	35.8	387	1	THIK_SALTY
9	54	35.8	390	1	THIK_PSEFR
10	52	34.4	387	1	THIK_YERPE
11	51	33.8	237	1	OXAA_PROMI
12	51	33.8	656	1	ACSA_SYNEL
13	50	33.1	887	1	IF2_CHLCV
14	49	32.5	890	1	IF2_CHLGN
15	49	32.5	892	1	IF2_CHLTR
16	49	32.5	896	1	IF2_CHLMU
17	48	31.8	539	1	TCPD_HUMAN
18	48	31.8	539	1	TCPD_MOUSE
19	48	31.8	601	1	SG2_FANRI
20	48	31.8	605	1	DY14_HUMAN
21	47	31.1	528	1	TCPD_YEAST
22	47	31.1	533	1	TCPD_AEDTR
23	47	31.1	880	1	IF2_LEPIN
24	46.5	30.8	350	1	CMTG_PSEPU
25	46	30.5	536	1	TCPD_FUGRU
26	46	30.5	874	1	SYA_PASMU
27	45	29.8	281	1	VPM_BPHPL
28	45	29.8	358	1	RNFD_RHOCA
29	45	29.8	360	1	CGST_PSEPK
30	45	29.8	401	1	CAIF_ACICA
31	45	29.8	401	1	PCAF_ACICA
32	45	29.8	415	1	PGK_SULTO
33	45	29.8	429	1	PUR2_VIBCH

34 45 29.8 431 1 PUR2_XANCP
35 45 29.8 440 1 ZM10_HUMAN
36 45 29.8 529 1 YB53_METH
37 45 29.8 829 1 IF2_HAEIN
38 45 29.8 1248 1 NLFA_DROME
39 44.5 29.5 521 1 TRPE_BUCAI
40 44.5 29.5 838 1 PTF1_XANCP
41 44 29.1 272 1 RFXA_HUMAN
42 44 29.1 329 1 Y146_HAEIN
43 44 29.1 407 1 KIM2_MOUSE
44 44 29.1 543 1 THSB_THEAC
45 44 29.1 628 1 GIDA_WIGBR

Q8pd48 xanthomonas
O75800 homo sapien
O27221 methanobact
P44323 haemophilus
Q86np2 brochella
Q44695 buchnera ap
P45597 x multiphos
O00287 homo sapien
P44542 haemophilus
Q62168 mus musculu
P48425 thermoplasm
Q8d3k0 wiggleswort

ALIGNMENTS

RESULT 1
IKKB_HUMAN
ID IKKB_HUMAN STANDARD; PRT; 756 AA.
AC O14920; O75327; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkkappaB kinases essential for
RT NF-kappaB activation.";
RN Science 278:860-866 (1997).
[2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Cao X., Cao Z., Rothe M., Goeddel D.V.;
RT "IkkappaB kinase-beta: NF-kappaB activation and complex formation with
RT Science 278:866-869 (1997).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RN Gene 222:31-40 (1998).
[4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of IkkappaB kinase beta (IKKB) to human chromosome band
RT 8p12-->p11 by in situ hybridization.";
RN Cytogenet. Cell Genet. 82:32-33 (1998).
[5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [16]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RT Mol. Cell. Biol. 18:7336-7343(1998).
RL [7]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RT Am. J. Physiol. 278:C451-C462(2000).
RN [18]
RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKBG.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RA "Regulation of SRC-3 (pCIP/ACTE/ATB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RT Mol. Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (by similarity).
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-alpha-p65-p50
CC complex. Phosphorylated IKB-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -!- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC -----
CC EMBL; AF029684; AAC51860.1; -;
CC EMBL; AF080158; AAD08997.1; -;
CC EMBL; AF031416; AAC64675.1; -;
CC EMBL; BC006231; AAH06231.1; -;
CC HSP; Q63450; IAO6.
CC Genew; HGNC:5960; IKKBK.
CC MIM; 603258; -;
CC GO; GO:0005737; C:cytoplasm; NAS.
CC GO; GO:0005524; F:ATP binding; NAS.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT NP_BIND 21 29 NEMO-BINDING.
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 ATP (BY SIMILARITY).
FT MOD_RES 23 23 BY SIMILARITY.
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
FT MUTAGEN 177 177 EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT CONFLICT 231 255 WHSKVRQKSEVDIVVSEDLNGTVKF -> CVERMFGTVVAHS
FT CONFLICT 425 425 CNPSTLGGGRWI (IN REF. 5).
FT CONFLICT Q -> H (IN REF. 1).
SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9B14E CRC64;
Query Match 100.0%; Score 151; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 4.1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
DB 535 ERMALQTDIVDLQSPMGKQGGTLDLLE 564
RESULT 2
IKKB MOUSE STANDARD; PRT; 757 AA.
ID IKKB MOUSE STANDARD; PRT; 757 AA.
AC Q88351; Q9R1J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=9818238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of IKB.";
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

[3]
 RN DEVELOPMENTAL STAGE
 RP MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-I., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 [4]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 [5]
 RN
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBK
 CC and CREBBP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -!- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.

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 DR EMBL; AF026524; AAC23557.1; -.
 DR EMBL; AF088910; AAD52095.1; -.
 DR HGSP; Q63450; IAO6.
 DR MGD; MGI:1338071; Ikbb.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).

FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 736 TLDWSLQMEDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449CSE CRC64;
 Query Match 100.0%; Score 151; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 4.1e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ERMALQTDIVDLQSPMGRKQGGLDLDLE 30
 Db 535 ERMALQTDIVDLQSPMGRKQGGLDLDLE 564
 RESULT 3
 ID IKKB RAT STANDARD; PRT; 757 AA.
 AC Q9QI78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 26-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBK
 CC and CREBBP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.

```

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF115282; AAF21978.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR Transfrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 757 AA; 86866 MW; 3APFE46A7DF91P9C CRC64;
Query Match 100.0%; Score 151; DB 1; Length 757;
Best Local Similarity 100.0%; Pred. No. 4.1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERMALQTDIVDLQRSPGMRKQGGLDLDLE 30
Db 535 ERMALQTDIVDLQRSPGMRKQGGLDLDLE 564
RESULT 4
IKKA_MOUSE
ID IKKA_MOUSE STANDARD; PRT; 745 AA.
AC Q6080; Q9D2X3.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)
DE (I kappa-B kinase alpha) (IKKalpha) (IKK-alpha) (IkappaB kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).
DE CHUK OR IKKA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=BALB/c;
RX MEDLINE=9604444; PubMed=7558004;
RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
RT chromosome 10 and mouse chromosome 19."
RL Genomics 27:348-351 (1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=BALB/c;
RX MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase

```

```

RT catalytic domain."
RL Cell. Mol. Biol. Res. 41:537-549 (1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217951;
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saico R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=20198447; PubMed=10733566;
RA McKenzie F.R., Connelly M.A., Ballarano D., Mueller J.R.,
RA Gelezianas R., Marcu K.B.;
RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
RT IKKbeta have different activation requirements."
RL Mol. Cell. Biol. 20:2635-2649 (2000).
RN [5]
RP PHOSPHORYLATION BY MAP3K14/NIK.
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542 (1998).
RN [6]
RP IKKA-IKKB BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
RT IKKbeta subunit phosphorylation."
RL Science 284:309-313 (1999).
RN [7]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., Dibonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase."
RL Mol. Cell. Biol. 18:7336-7343 (1998).
RN [8]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection."
RL Am. J. Physiol. 278:C451-C462 (2000).
CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -I- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC when dephosphorylated.
CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.

```

CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-p65-p50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKK1, IKK2 and CRBBP (By
 CC similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1;

CC IsoId=Q0680-1; Sequence=Displayed;

CC Name=2; Synonyms=Delta LH;

CC IsoId=Q0680-2; Sequence=VSP_004866, VSP_004867;

CC Name=3; Synonyms=Delta H;

CC IsoId=Q0680-3; Sequence=VSP_004868, VSP_004869;

CC -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.

CC -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.

CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC IKAPPAB KINASE SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).

CC ENBL; U12473; AAC52589.1; --

CC ENBL; AK018671; BAB31335.1; --

CC PIR; I49101; I49101.

CC HSP; Q63450; I406.

CC MGD; MGI:99484; Chuk.

CC InterPro: IPR000719; Prot kinase.

CC InterPro: IPR008271; Ser_Thr_kinase.

CC InterPro: IPR001245; Tyr_kinase.

CC Pfam; PF00069; pkinase; 1.

CC PRINTS; PR00109; TYRKINASE.

CC ProDom; PD000001; Prot kinase; 1.

CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.

CC PROSITE; PS00108; PROTEIN KINASE ST; 1.

CC PROSITE; PS00011; PROTEIN KINASE_DOM; 1.

CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC phosphorylation; Alternative splicing.

CC FT DOMAIN 15 300 PROTEIN KINASE.

CC FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).

CC FT DOMAIN 738 743 NEMO-BINDING.

CC FT NP_BIND 21 29 ATP (BY SIMILARITY).

CC FT BINDING 44 44 ATP (BY SIMILARITY).

CC FT ACT_SITE 144 144 BY SIMILARITY.

CC FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)

CC FT MOD_RES 176 176 (BY SIMILARITY).

CC FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)

CC FT VARSPLIC 452 471 MSLRLRNANUTRMKNTLS -> IFRNVKSMERNRKGKH

CC FT SLE (in isoform 2).

CC FT FTId=VSP_004866.

CC FT Missing (in isoform 2).

CC FT Missing (in isoform 2).

CC FT FTId=VSP_004867.

CC FT DMLVSDST -> GKTLSQY (in isoform 3).

CC FT FTId=VSP_004868.

CC FT Missing (in isoform 3).

CC FT FTId=VSP_004869.

CC FT K -> E (IN REF. 3).

CC FT S -> Y (IN REF. 3).

CC FT SEQUENCE 745 AA; 84728 MW; 3FEF582AFF92233 CRC64;

CC Query Match 55.6%; Score 84; DB 1; Length 745;

CC Best Local Similarity 46.7%; Pred. No. 6.9e-05;

Matches 14; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 ERMALQTDIVLQSPMGKQGGTLDLLE 30
 Db 532 DQIMSLATEIMELQSPYGRGQGLMESLE 561

RESULT 5

IKKA HUMAN

ID IKKA HUMAN STANDARD; PRT; 745 AA.

AC O15111; O14666; Q13132; Q92467;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)

DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkkappaB kinase)

DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous

DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KA).

GN CHUK OR IKKA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.

RP TISSUE=T-cell;

RC MEDLINE=97386461; PubMed=9244310;

RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;

RT "Identification and characterization of an IkappaB kinase.";

RL Cell 90:373-383(1997).

[2]

RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RP MEDLINE=97394468; PubMed=9252186;

RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;

RT "A cytokine-responsive IkappaB kinase that activates the transcription

RT factor NF-kappaB.";

RL Nature 388:548-554(1997).

[3]

RN SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND

RP SER-176.

RC TISSUE=Cervical carcinoma;

RX MEDLINE=98008813; PubMed=9346484;

RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,

RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;

RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for

RT NF-kappaB activation.";

RL Science 278:860-866(1997).

[4]

RN SEQUENCE FROM N.A.

RP TISSUE=Heart;

RC MEDLINE=99032998; PubMed=9813230;

RA Hu M.C.-T., Wang Y.-P.;

RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and

RT embryonic tissues but localized to different human chromosomes.";

RL Gene 222:31-40(1998).

[5]

RN SEQUENCE OF 32-745 FROM N.A.

RP TISSUE=Cervical carcinoma;

RX MEDLINE=96258427; PubMed=8777433;

RA Connolly M.A., Marcu K.B.;

RT "CHUK, a new member of the helix-loop-helix and leucine zipper

RT families of interacting proteins, contains a serine-threonine kinase

RT catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1995).

[6]

RN PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179

RP AND SER-180.

RX MEDLINE=98188283; PubMed=9520446;

RA Ling L., Cao Z., Goeddel D.V.;

RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of

RT Ser-176.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

[7]

RN

RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=994113720; PubMed=10485710; Pfeiffer S.R., Pfeiffer L.M.,
 RA Oznes O.N., Mayo L.D., Gustin J.A.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase";
 RL Nature 401:82-85(1999).
 RN [8];
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RA "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation";
 RL Science 284:309-313(1999).
 RN [9];
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10];
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11];
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; IKKB AND IKKKB.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RA "Regulation of SRC-3 (pCIP/ACTR/ATB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAPK14/NIK, MEK1, IKAP and IKB-alpha-p65-p50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC
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 CC -----
 DR EMBL: AF012890; AAC51662.1; -;
 DR EMBL: AF009225; AAC51671.1; -;
 DR EMBL: AF080157; RAD08996.1; -;
 DR EMBL: U22512; AAC50713.1; -;
 DR HSSP: Q63450; 1A06.
 DR Genew: HGNC:1974; CHUK.
 DR MIM: 600664; -;
 DR GO: GO:0005737; C:cytoplasm; TAS.
 DR GO: GO:0008384; F:IkappaB kinase activity; TAS.
 DR GO: GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR GO: GO:0007252; P:I-kappaB phosphorylation; TAS.
 DR GO: GO:0006955; P:immune response; TAS.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
 FT ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS -> DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 52.3%; Score 79; DB 1; Length 745;
 Best Local Similarity 43.3%; Pred. No. 0.0004; Mismatches 6; Indels 0; Gaps 0;
 Matches 13; Conservative 11;
 QY 1 ERMALQTDIVDLQSPMGKQGGTLDLIE 30
 DB 532 DQIMSLHAEIMELQKSPYGRGQDLMSLE 561
 RESULT 6
 THIK ECO57
 ID THIK ECO57 STANDARD; PRT; 387 AA.
 AC Q8X574;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
 DE subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
 GN FADA OR Z6366 OR ECS4773.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";

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RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba I., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: FadB and fadA are the alpha and beta subunits of the
CC multifunctional enzyme complex of the fatty acid degradation
CC cycle. (By similarity).
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
CC -!- SUBUNIT: Tetramer of two alpha chains and two beta chains (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thiolase family.
CC
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CC
CC -----
CC EMBL; AE005615; AAG59039.1; -.
CC EMBL; AP002567; BAB38196.1; -.
CC PIR; C86072; C86072.
CC PIR; E91225; E91225.
CC InterPro; IPR002155; Thiolase.
CC Pfam; PF00108; Thiolase; 1.
CC DR PROSITE; PS00098; THIOLEASE_1; 1.
CC DR PROSITE; PS00737; THIOLEASE_2; 1.
CC DR PROSITE; PS00099; THIOLEASE_3; 1.
CC Complete proteome.
CC Fatty acid metabolism; Transferase; Acyltransferase;
KW
FT ACT_SITE 91 91 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 373 373 BASE (BY SIMILARITY).
FT ACT_SITE 387 AA; 40841 MW; 98D3879B30B46CCC CRC64;
SQ SEQUENCE 387 AA; 40841 MW; 98D3879B30B46CCC CRC64;
Query Match 35.8%; Score 54; DB 1; Length 387;
Best Local Similarity 61.1%; Pred. No. 1.3;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 7 QTDIVDLQRSPMGRKQGS 24
Db 3 QVIVDAIRTPMGRSGG 20
RESULT 7
THIK_ECOLI STANDARD; PRT; 387 AA.
AC P21151; P78130;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
DE subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
GN FADA OR OLDA OR B3845.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;

```

```

RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RT from 84.5 to 86.5 minutes.";
RL Science 257:771-778(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91035260; PubMed=1699931;
RA Dirusso C.C.;
RT "Primary sequence of the Escherichia coli fadBA operon, encoding the
RT fatty acid-oxidizing multienzyme complex, indicates a high degree of
RT homology to eucaryotic enzymes.";
RL J. Bacteriol. 172:6459-6468(1990).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=90285166; PubMed=2191949;
RA Yang S.-Y., Yang X.-Y.H., Healy-Louie G., Schulz H., Elzinga M.;
RT "Nucleotide sequence of the fadA gene. Primary structure of
RT 3-ketoacyl-coenzyme A thiolase from Escherichia coli and the
RT structural organization of the fadAB operon.";
RL J. Biol. Chem. 265:10424-10429(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=90370500; PubMed=2204034;
RA Nakahigashi K., Inokuchi H.;
RT "Nucleotide sequence of the fadA and fadB genes from Escherichia
RT coli.";
RL Nucleic Acids Res. 18:4937-4937(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- FUNCTION: FadB and fadA are the alpha and beta subunits of the
CC multifunctional enzyme complex of the fatty acid degradation
CC cycle.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
CC -!- SUBUNIT: Tetramer of two alpha chains and two beta chains.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the thiolase family.
CC
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CC
CC -----
CC EMBL; M87049; AAA67642.1; -.
CC EMBL; M59368; AAA23751.1; -.
CC EMBL; X52837; CAB40810.1; -.
CC EMBL; M74164; AAA62778.1; -.
CC EMBL; AE000460; AAC76848.1; -.
CC PIR; P65189; XUEC.
CC HSP; P27796; IAFY.
CC ECO2DBASE; H038.6; 6TH EDITION.
CC ECO2DBASE; H038.7; 6TH EDITION.
CC EcoGene; EG10278; fadA.
CC InterPro; IPR002155; Thiolase.
CC Pfam; PF00108; Thiolase; 1.
CC DR PROSITE; PS00098; THIOLEASE_1; 1.
CC DR PROSITE; PS00099; THIOLEASE_3; 1.
CC DR PROSITE; PS00737; THIOLEASE_2; 1.
CC Fatty acid metabolism; Transferase; Acyltransferase;
KW

```

Complete proteome. 91 SUBSTRATE BINDING (BY SIMILARITY).
 FT ACT SITE 373 373 BASE (BY SIMILARITY).
 FT ACT SITE 373 373 T -> S (IN REF. 2 AND 3).
 FT CONFLICT 37 37 E -> G (IN REF. 4).
 FT CONFLICT 119 119 TMCI -> DGCVS (IN REF. 3).
 FT CONFLICT 371 374 TMCI -> DGCVS (IN REF. 3).
 SQ SEQUENCE 387 AA; 40890 MW; CB0FFBEP4597D8BA CRC64;
 Query Match 35.8%; Score 54; DB 1; Length 387;
 Best Local Similarity 61.1%; Pred. No. 1.3;
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 7 QTDIVDLQSPMGKQGG 24
 Db 3 QQVIVDAIRTPMGSKG 20
 RESULT 8
 THIK_SALTY STANDARD; PRT; 387 AA.
 ID THIK_SALTY STANDARD; PRT; 387 AA.
 AC Q9L6L6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DT 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty acid oxidation complex beta subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
 DE DE subunit)
 GN FADA OR STM3982 OR STM1.7 OR STY3578 OR T3316.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 CN NCBI_TaxID=602, 601;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
 RA "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
 RT Nature 413:852-856(2001).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S.typhi; STRAIN=CT18;
 RC MEDLINE=21534947; PubMed=11677608;
 RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connor P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;
 RA "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18";
 RT Nature 413:848-852(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
 RC MEDLINE=22531367; PubMed=12644504;
 RX Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodyolanni V., Schwartz D.C., Blattner F.R.;
 RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
 RT J. Bacteriol. 185:2330-2337(2003).
 RL J.
 CC -!- FUNCTION: PadB and fadA are the alpha and beta subunits of the multifunctional enzyme complex of the fatty acid degradation cycle [By similarity].
 CC -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
 CC -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
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 CC -----
 DR EMBL; D10390; BAA01228.1; -.
 DR PIR; JS0624; JS0624.
 DR HSP; P27796; IPIXT.
 DR InterPro; IPR002155; Thiolase.
 DR Pfam; PF00108; thiolase; 1.
 DR Pfam; PF02803; thiolase; 1.
 DR PROSITE; PS00098; THIOLEASE_1; 1.
 DR PROSITE; PS00099; THIOLEASE_3; 1.
 DR PROSITE; PS00737; THIOLEASE_2; 1.
 KW Fatty acid metabolism; Transferase; Acyltransferase.
 FT INIT MET 0
 FT ACT SITE 94 94 SUBSTRATE BINDING (BY SIMILARITY).
 FT ACT SITE 376 376 BASE (BY SIMILARITY).
 SQ SEQUENCE 390 AA; 41475 MW; F9270235BCBE3D09 CRC64;
 Query Match 35.8%; Score 54; DB 1; Length 390;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 10 IVDLQSPMGKRGKG 24
 DB 9 IVDLQSPMGKRGKG 24
 RESULT 10
 THIK YERPE
 ID THIK YERPE STANDARD; PRT; 387 AA.
 AC QSZAM9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
 DE subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
 GN FADA OR YPO3767 OR Y0463.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feitwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
 RA Stanmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 CC -1- FUNCTION: FadB and fadA are the alpha and beta subunits of the
 CC multifunctional enzyme complex of the fatty acid degradation
 CC cycle (By similarity).
 CC -1- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
 CC -1- PATHWAY: Fatty acid beta-oxidation cycle; third step.

CC -1- SUBUNIT: Tetramer of two alpha chains and two beta chains (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thiolase family.
 CC -----
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 CC -----
 DR EMBL; AJ414158; CAC93235.1; -.
 DR EMBL; AE013646; AAM84052.1; -.
 DR PIR; AG0458; AG0458.
 DR InterPro; IPR002155; Thiolase.
 DR Pfam; PF00108; thiolase; 1.
 DR Pfam; PF02803; thiolase; 1.
 DR PROSITE; PS00098; THIOLEASE_1; 1.
 DR PROSITE; PS00737; THIOLEASE_2; 1.
 DR PROSITE; PS00099; THIOLEASE_3; 1.
 KW Fatty acid metabolism; Transferase; Acyltransferase;
 KW Complete proteome.
 FT ACT SITE 91 91 SUBSTRATE BINDING (BY SIMILARITY).
 FT ACT SITE 373 373 BASE (BY SIMILARITY).
 SQ SEQUENCE 387 AA; 40917 MW; 1690502C07AE9F63 CRC64;
 Query Match 34.4%; Score 52; DB 1; Length 387;
 Best Local Similarity 60.0%; Pred. No. 2.6;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 10 IVDLQSPMGKRGKG 24
 DB 6 IIDAVRTPMGKRGKG 20
 RESULT 11
 ID OXAA PROMI STANDARD; PRT; 237 AA.
 AC P22833;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Inner membrane protein oxaA (fragment).
 DE OXAA.
 GN Proteus mirabilis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Proteus.
 OX NCBI_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LM1509;
 RX MEDLINE=91033012; PubMed=2172087;
 RA Skovgaard O.;
 RT "Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to
 RL the 60X-rnpA-rnpH-dnaA-dnaN-recF-gyrB region of Escherichia coli."
 RL Gene 93:27-34(1990).
 CC -1- FUNCTION: Required for the insertion of integral membrane proteins
 CC into the membrane. Probably plays an essential role in the
 CC integration of proteins of the respiratory chain complexes.
 CC Involved in integration of membrane proteins that insert
 CC independently and independently of the Sec translocase complex (By
 CC similarity).
 CC -1- SUBUNIT: Specifically interacts with transmembrane segments of
 CC nascent integral membrane proteins during membrane integration (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the OXA1/oxaA family. Subfamily 1.
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CC -----
 DR EMBL; M58352; AAA83954.1; -;
 DR PIR; J00729; J00729;
 DR HAMAP; MF_01810; -; 1;
 DR InterPro; IPR001708; 60kDa_innermemb.
 DR PRINTS; PR00701; 60KDINNERMP.
 KW Transmembrane; Inner membrane.
 FT TRANSMEM 7 23 POTENTIAL.
 FT NON_TER 237 237
 SQ SEQUENCE 237 AA; 26664 MW; 07FCC405B9DB3F36 CRC64;

Query Match 33.8%; Score 51; DB 1; Length 237;
 Best Local Similarity 31.0%; Pred. No. 2.2;
 Matches 9; Conservative 12; Mismatches 4; Indels 4; Gaps 1;

QY 2 RMVALQTDIVLQSPMGKRGKGGTLDLLE 30
 DB 61 KLITVKTVDLDIRIN----TQGGTIDEAD 85

RESULT 12
 ID ACSEA_SYNEEL STANDARD; PRT; 656 AA.
 AC Q8DKH2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
 DE activating enzyme).
 GN ACSEA OR TLL0887.
 OS Synecococcus elongatus (Thermosynechococcus elongatus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32046;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BP-1;
 RX MEDLINE=22225144; PubMed=12240834;
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
 RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the thermophilic cyanobacterium
 RT Thermosynechococcus elongatus BP-1.";
 RL DNA Res. 9:123-130(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
 CC acetyl-CoA.

CC -!- PTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase
 CC activates the enzyme (By similarity).
 CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 CC family.

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CC -----
 DR EMBL; AP005372; BAC08439.1; -;
 DR HAMAP; MF_01123; -; 1;
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00455; AMP BINDING; 1.
 KW Ligase; Acetylation; Complete proteome.
 FT ACT_SITE 529 529 BY SIMILARITY.
 FT MOD_RES 621 621 ACETYLATION (BY SIMILARITY).

SQ SEQUENCE 656 AA; 73164 MW; 73462DCAF43F8ED2 CRC64;
 Query Match 33.8%; Score 51; DB 1; Length 656;
 Best Local Similarity 50.0%; Pred. No. 6.6;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 9 DIVLQSPMGKRGKGGTLL 26
 DB 454 DVDVLEGNFVGVNEGGL 471

RESULT 13
 ID IF2_CHLCV STANDARD; PRT; 887 AA.
 AC Q823F2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Translation initiation factor IF-2.
 GN INFB OR CCA00465.
 OS Chlamydomophila caviae.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.

OC NCBI_TaxID=83557;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=GPIC;
 RX MEDLINE=22569155; PubMed=12682364;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
 RA Heidelberg J., Holtzapfle E., Khouri H., Federova N.B., Carty H.A.,
 RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
 RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
 RA Fraser C.M.;

RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
 RT examining the role of niche-specific genes in the evolution of the
 RT Chlamydiaceae.";
 RL Nucleic Acids Res. 31:2134-2147(2003).

CC -!- FUNCTION: One of the essential components for the initiation of
 CC protein synthesis. Protects formylmethionyl-tRNA from spontaneous
 CC hydrolysis and promotes its binding to the 30S ribosomal subunits.
 CC Also involved in the hydrolysis of GTP during the formation of the
 CC 70S ribosomal complex (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the IF-2 family.

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CC -----
 DR EMBL; AE016995; AAP05210.1; -;
 DR TIGR; CCA00465; -;
 DR HAMAP; MF_00100; -; 1;
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR004161; EFTU_D2.

DR InterPro; IPR000178; IF2.
 DR InterPro; IPR006847; IF2_N.
 DR InterPro; IPR005225; Small_GTP.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 2.
 DR Pfam; PF04760; IF2_N; 1.

DR ProDom; PD186100; IF2; 1;
 DR TIGRPFAMs; TIGR00487; IF-2; 1.
 DR TIGRPFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS01176; IF2; 1.
 KW Initiation factor; Protein biosynthesis; GTP-binding;
 Complete proteome.
 FT DOMAIN 396 544 G-DOMAIN
 FT NP_BIND 402 409 GTP (BY SIMILARITY).
 FT NP_BIND 448 452 GTP (BY SIMILARITY).


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DR EMBL; AE001283; AAC67687.1; -.
DR PIR; H71558; H71558.
DR HAMAP; MF_00100; -.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000178; IF2_N.
DR InterPro; IPR006847; IF2_N.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 2.
DR Pfam; PF04760; IF2_N; 1.
DR ProDom; PDL86100; IF2; 1.
DR TIGRFAMs; TIGR00487; IF-2; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01176; IF2; 1.
KW Initiation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT DOMAIN 400 548 G-DOMAIN
FT NP_BIND 406 413 GTP (BY SIMILARITY).
FT NP_BIND 452 456 GTP (BY SIMILARITY).
FT NP_BIND 506 509 GTP (BY SIMILARITY).
SQ SEQUENCE 892 AA; 97009 MW; 9D401C079D6B1A51 CRC64;

Query Match 32.5%; Score 49; DB 1; Length 892;
Best Local Similarity 38.1%; Pred. No. 19;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 3 MMALQTDIVDLQSPMGKQG 23
Db 555 MLALQAEVLELKADPSARARG 575

```

Search completed: September 24, 2004, 09:43:34
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:58 ; Search time 116 Seconds
(without alignments)
81.600 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERMALQTDIVDLQSPMGRKQGGLDLE 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_xvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	100.0	756	6 Q95KV0	Q95kv0 bos taurus
2	84	55.6	584	11 Q80VU2	Q80vu2 mus musculus
3	84	55.6	740	6 Q95KV1	Q95kv1 bos taurus
4	84	55.6	745	11 Q8CBT3	Q8cbt3 mus musculus
5	83	55.0	758	13 Q7ZTU1	Q7ztu1 brachydanio
6	66.5	44.0	732	5 Q61565	Q61565 crassostrea
7	56	37.1	465	2 Q9AP21	Q9ap21 pseudomonas
8	56	37.1	465	16 Q88DF2	Q88df2 pseudomonas
9	55	36.4	283	2 Q9X6F2	Q9x6f2 pseudomonas
10	55	36.4	283	16 Q9HVL1	Q9hvl1 pseudomonas
11	55	36.4	283	16 Q87VU13	Q87vu13 pseudomonas
12	55	36.4	533	10 Q9ZEX1	Q9zrx1 glycine max
13	54	35.8	387	16 Q8FBI3	Q8fbi3 escherichia
14	54	35.8	387	16 Q83PG2	Q83pg2 shigella fl
15	54	35.8	391	2 Q93Q11	Q93q11 pseudomonas
16	54	35.8	391	2 Q9R9W0	Q9r9w0 pseudomonas

17	54	35.8	391	16 Q9HZJ3	Q9hzj3 pseudomonas
18	54	35.8	391	16 Q88L01	Q88l01 pseudomonas
19	54	35.8	391	16 Q87ZB3	Q87zb3 pseudomonas
20	53.5	35.4	1710	5 Q9V9N7	Q9v9n7 drosophila
21	53	35.1	387	16 Q9KN10	Q9kn10 vibrio chol
22	53	35.1	387	16 Q8DDK5	Q8ddk5 vibrio vuln
23	52.5	34.8	649	10 Q9AW00	Q9aw00 guillardia
24	52	34.4	387	2 Q9F0Y6	Q9f0y6 enterobacte
25	52	34.4	391	16 Q87TP0	Q87tp0 vibrio para
26	51	33.8	174	10 Q7XBP1	Q7xbp1 chlorarachn
27	51	33.8	396	16 Q93JG7	Q93jg7 streptomyce
28	50.5	33.4	617	13 Q9PU64	Q9pu64 brachydanio
29	50.5	33.4	617	13 Q9IAA9	Q9iaa9 brachydanio
30	50.5	33.4	617	13 Q80AR6	Q80ar6 brachydanio
31	50.5	33.4	4317	16 Q88F56	Q88f56 pseudomonas
32	50	33.1	465	16 Q82XR0	Q82xr0 nitrosomona
33	49.5	32.8	297	16 Q9KE47	Q9ke47 bacillus ha
34	49	32.5	242	16 Q88IZ8	Q88iz8 pseudomonas
35	49	32.5	301	16 Q8DUQ1	Q8duq1 streptococc
36	49	32.5	401	16 Q7VV88	Q7vv88 bordetella
37	49	32.5	494	16 Q8F3M2	Q8f3m2 leptospira
38	49	32.5	536	10 Q8L994	Q8l994 arabidopsis
39	49	32.5	536	10 Q9LV21	Q9lv21 arabidopsis
40	49	32.5	676	2 Q07365	Q07365 chlamydia t
41	48.5	32.1	304	16 Q81MD1	Q81md1 bacillus an
42	48.5	32.1	304	16 Q818Z0	Q818z0 bacillus ce
43	48.5	32.1	351	2 Q8GI19	Q8gi19 gamma-prote
44	48.5	32.1	373	16 Q91I40	Q91i40 pseudomonas
45	48.5	32.1	373	16 Q88P67	Q88p67 pseudomonas

ALIGNMENTS

RESULT 1

Q95KV0 ID Q95KV0 PRELIMINARY; PRT; 756 AA.
AC Q95KV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IKB kinase-beta.
GN BIKKBETA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKBs) alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AJ414556; CAC93687.1;
DR GO: GO:0005324; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 100.0%; Score 151; DB 6; Length 756;

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Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKGGTLDLLE 30
DB 535 ERMALQTDIVDLQSPMGKGGTLDLLE 564

RESULT 2
Q80VU2
ID Q80VU2 PRELIMINARY; PRT; 584 AA.
AC Q80VU2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved helix-loop-helix ubiquitous kinase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018243; AAH18243.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 584 AA; 66805 MW; D99BB8A6DF1CA4EB CRC64;

Query Match 55.6%; Score 84; DB 11; Length 584;
Best Local Similarity 46.7%; Pred. No. 0.00024;
Matches 14; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKGGTLDLLE 30
DB 532 DQIMSLHTEIMELQSPYGRQGLMESLE 561

RESULT 3
Q95KV1
ID Q95KV1 PRELIMINARY; PRT; 740 AA.
AC Q95KV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ikb kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RA "Identification and characterisation of the bovine Ikb kinases (IKBs)
RT alpha, beta and gamma.";
```

```
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ414555; CAC93686.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PS00109; TYRKINASE.
DR PRODOM; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BELL1F44D176 CRC64;

Query Match 55.6%; Score 84; DB 6; Length 740;
Best Local Similarity 46.7%; Pred. No. 0.00032;
Matches 14; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKGGTLDLLE 30
DB 532 DQIMSLHTEIMELQSPYGRQGLMESLE 561

RESULT 4
Q8CBT3
ID Q8CBT3 PRELIMINARY; PRT; 745 AA.
AC Q8CBT3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved helix-loop-helix ubiquitous kinase.
GN CHUK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 50,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK035326; BAC29034.1; -.
DR MGD; MGI:99484; Chuk.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PS00109; TYRKINASE.
DR PRODOM; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;
```

Query Match 55.0%; Score 83; DB 13; Length 758;
Best Local Similarity 50.0%; Pred. No. 0.00047;

RT "A broad host range replicon with different requirements for
 RT replication initiation in three bacterial species.";

RL EMBO J. 20:3262-3271(2001).

DR EMBL; AF229444; AAK00231.1; -.

DR HSSP; P03005; LJWE.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0003678; F:DNA helicase activity; IEA.

DR GO; GO:000166; F:nucleotide binding; IEA.

DR GO; GO:0006260; P:DNA replication; IEA.

DR InterPro; IPR003593; AAA_Atpase.

DR InterPro; IPR007694; DnaB_C.

DR InterPro; IPR007692; DnaB_Helicase.

DR InterPro; IPR007693; DnaB_N.

DR Pfam; PF00772; DnaB_1.

DR Pfam; PF03796; DnaB_C_1.

DR ProDom; PD332834; DnaB_C_1.

DR SMART; SM00382; AAA; 1.

DR TIGRFAMs; TIGR00665; DnaB; 1.

KW ATP-binding; Helicase.

SQ SEQUENCE 465 AA; 51581 MW; 43A505CB32C20193 CRC64;

Query Match 37.1%; Score 56; DB 2; Length 465;

Best Local Similarity 37.9%; Pred. No. 4.5;

Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 RMVALQTDIVDLQSPMGKQGGTLLDLE 30

Db 127 QLISISTDIADNAFNPQGRNAAEILDDAE 155

RESULT 8

Q88DF2

ID Q88DF2 PRELIMINARY; PRT; 465 AA.

AC Q88DF2

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Replicative DNA helicase.

GN DnaB OR PP4873.

OS Pseudomonas putida (strain KT2440).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=160488;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22423060; PubMed=12534463;

RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,

RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,

RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,

RA Chris Lee P., Holtzapfle E., Scanlan D., Tran K., Moazzez A.,

RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,

RA Lauber J., Stjepandic D., Hohnsels J., Straetz M., Heim S.,

RA Kiewitz C., Eisen J., Timmis K.N., Dueterhoeft A., Tuemmler B.,

RA Fraser C.M.;

RT "Complete genome sequence and comparative analysis of the

RT metabolically versatile Pseudomonas putida KT2440.";

RL Environ. Microbiol. 4:799-808(2002).

DR EMBL; AE016792; AAN70442.1; -.

DR TIGR; PP4873; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0003678; F:DNA helicase activity; IEA.

DR GO; GO:0006260; P:DNA replication; IEA.

DR InterPro; IPR007694; DnaB_C.

DR InterPro; IPR007693; DnaB_N.

DR Pfam; PF00772; DnaB; 1.

DR Pfam; PF03796; DnaB_C_1.

KW Helicase; Complete proteome.

SQ SEQUENCE 465 AA; 51581 MW; 43A505CB32C20193 CRC64;

Query Match 37.1%; Score 56; DB 16; Length 465;

Best Local Similarity 37.9%; Pred. No. 4.5;

Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 RMVALQTDIVDLQSPMGKQGGTLLDLE 30

Db 127 QLISISTDIADNAFNPQGRNAAEILDDAE 155

RESULT 9

Q9X6F2

ID Q9X6F2 PRELIMINARY; PRT; 283 AA.

AC Q9X6F2

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE RpmA.

GN RpmA.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=4020;

RX MEDLINE=20231781; PubMed=10768936;

RA Simpson D.A., Speert D.P.;

RT "RpmA is required for nonopsonic phagocytosis of Pseudomonas

RT aeruginosa.";

RL Infect. Immun. 68:2493-2502(2000).

DR EMBL; AF136403; RAD33690.1; -.

SQ SEQUENCE 283 AA; 30740 MW; 4AA5DAC6957C0693 CRC64;

Query Match 36.4%; Score 55; DB 2; Length 283;

Best Local Similarity 46.4%; Pred. No. 3.6;

Matches 13; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLLD 28

Db 91 EGMMAIEADIEDPAASPIFSKYPGVLD 118

RESULT 10

Q9HUL1

ID Q9HUL1 PRELIMINARY; PRT; 283 AA.

AC Q9HUL1

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Chemotaxis protein MotA.

GN MOTA OR PA4954.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PAO1;

RX MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT opportunistic pathogen.";

RL Nature 406:959-964(2000).

DR EMBL; AE004908; AAG08339.1; -.

DR PIR; H83026; H83026.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0003774; F:motor activity; IEA.

DR GO; GO:0008565; F:protein transporter activity; IEA.

DR GO; GO:0006935; P:chemotaxis; IEA.

DR GO; GO:0001539; P:ciliary/flagellar motility; IEA.

DR GO; GO:0006810; P:transport; IEA.

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DR InterPro: IPR000540; Flag_MotA.
DR InterPro: IPR002898; MotA_ExtB.
DR Pfam: PF01618; MotA_ExtB; 1.
DR PROSITE; PS01307; MOT_A; 1.
DR Complete proteome.
SQ SEQUENCE 283 AA; 30094 MW; 9741C163CC63687B CRC64;

Query Match 36.4%; Score 55; DB 16; Length 283;
Best Local Similarity 46.4%; Pred. No. 3.6; Mismatches 12; Indels 0; Gaps 0;
Matches 13; Conservative 3;

QY 1 ERMALQTDIVDLQSPMRKQGGLDD 28
| | | | | | | | | | | | | | | | | |
Db 91 EGMWAIEDIEDPAASPIFYKPGVLKD 118

RESULT 11
Q87VI3 PRELIMINARY; PRT; 283 AA.
AC Q87VI3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemotaxis motA protein.
GN MOTA-2 OR PSPTO4953.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Barry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson K., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae."
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016873; AA058391.1; -.
DR TIGR; PSPTO4953; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0001539; P:ciliary/flagellar motility; IEA.
DR InterPro: IPR000540; Flag_MotA.
DR PROSITE; PS01307; MOT_A; 1.
DR Complete proteome.
SQ SEQUENCE 283 AA; 30193 MW; C6340C897E4D03C7 CRC64;

Query Match 36.4%; Score 55; DB 16; Length 283;
Best Local Similarity 46.4%; Pred. No. 3.6; Mismatches 12; Indels 0; Gaps 0;
Matches 13; Conservative 3;

QY 1 ERMALQTDIVDLQSPMRKQGGLDD 28
| | | | | | | | | | | | | | | | | |
Db 91 EGMWAIEDIEDPAASPIFYKPGVLKD 118

RESULT 12
Q92RX1 PRELIMINARY; PRT; 533 AA.
AC Q92RX1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytosolic chaperonin, delta-subunit.
GN CCTD.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. M103;
RA Tran Thi Phuong L., Nguyen Huy H., Chu Hoang H., Dinh Duy K.,
RA Nong Van H., Le Thi M.;
RT "Cloning of a cytosolic chaperonin gene from high-temperature tolerant
soybean cultivar M103.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ012318; CAA09989.1; -.
DR HSSP; P48424; 1A6D.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR InterPro: IPR002194; Chaperonin_TCP-1.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR InterPro: IPR008950; GroEL-ATPase.
DR InterPro: IPR001092; Hsp60/TCPI_1.
DR Pfam; PF00118; cpn60_TCPI_1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00750; TCPI_1; 1.
DR PROSITE; PS00995; TCPI_3; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 533 AA; 57573 MW; EF4E5D2E8D190AF2 CRC64;

Query Match 36.4%; Score 55; DB 10; Length 533;
Best Local Similarity 46.2%; Pred. No. 7.5; Mismatches 6; Indels 0; Gaps 0;
Matches 12; Conservative 6;

QY 5 ALQTDIVDLQSPMRKQGGLDDLE 30
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Db 190 APKPDVMDLRDVKIVKLGTVDDTE 215

RESULT 13
Q8FBI3 PRELIMINARY; PRT; 387 AA.
AC Q8FBI3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3-ketoacyl-CoA thiolase (EC 2.3.1.16).
GN KDA OR C4792.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016770; AAN83225.1; -.
DR GO; GO:0003988; F:acetyl-CoA C-acyltransferase activity; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004812; F:RNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR InterPro: IPR002155; Thiolase.
DR InterPro: IPR001412; tRNA-synt_1.
DR Pfam; PF00108; thiolase; 1.
DR Pfam; PF02803; thiolase C; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
DR PROSITE; PS00098; THIOLASE_1; 1.
DR PROSITE; PS00737; THIOLASE_2; 1.

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DR PROSITE; PS00099; THIOLASE 3; 1.
KW Acyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 387 AA; 40775 MW; 505E4A821C40C007 CRC64;

Query Match 35.8%; Score 54; DB 16; Length 387;
Best Local Similarity 61.1%; Pred. No. 7.5;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 QTDDIVDLQSPMGKQGG 24
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DB 3 QVVIYDAIRTPMGSKGG 20

RESULT 14
Q33PG2 PRELIMINARY; PRT; 387 AA.
ID Q83PG2;
AC Q83PG2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fatty acid oxidizing complex (Thiolase I, 3-ketoacyl-CoA thiolase,
DE acetyl-CoA transferase).
GN PADA OR SF3921 OR S3831.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
RN [3]
DR EMBL; AF015399; AAN45356.1; -;
DR EMBL; AF016990; RAP18842.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004812; F:RNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR InterPro; IPR002155; Thiolase.
DR InterPro; IPR001412; tRNA-synt_I.
DR Pfam; PF01108; thiolase; 1.
DR Pfam; PF02803; thiolase_C; 1.
DR PROSITE; PS00178; AA TRNA LIGASE_I; 1.
DR PROSITE; PS00098; THIOLASE_1; 1.
DR PROSITE; PS00737; THIOLASE_2; 1.
DR PROSITE; PS00099; THIOLASE_3; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 387 AA; 40846 MW; AE706AE0C8C0B0F0 CRC64;

Query Match 35.8%; Score 54; DB 16; Length 387;
Best Local Similarity 61.1%; Pred. No. 7.5;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 QTDDIVDLQSPMGKQGG 24
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DB 3 QVVIYDAIRTPMGSKGG 20

RESULT 15
Q33Q11 PRELIMINARY; PRT; 391 AA.
ID Q93Q11;
AC Q93Q11;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Beta-ketothiolase Fada.
GN PADA.
OS Pseudomonas oleovorans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=301;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC29347;
RA Fiedler S., Steinbuechel A., Rehm B.H.A.;
RT "fada genes from Pseudomonas oleovorans ATCC29347.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288535; AAK83059.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004812; F:RNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR InterPro; IPR002155; Thiolase.
DR InterPro; IPR001412; tRNA-synt_I.
DR Pfam; PF01108; thiolase; 1.
DR Pfam; PF02803; thiolase_C; 1.
DR PROSITE; PS00178; AA TRNA LIGASE_I; 1.
DR PROSITE; PS00098; THIOLASE_1; 1.
DR PROSITE; PS00737; THIOLASE_2; 1.
SQ SEQUENCE 391 AA; 41645 MW; D7CAE2F37ED170A1 CRC64;

Query Match 35.8%; Score 54; DB 2; Length 391;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 IVDLQSPMGKQGG 24
| | | | | : | | | | : | |
DB 10 IVDLQSPMGKQGG 24

Search completed: September 24, 2004, 09:45:37
Job time : 119 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:59 ; Search time 18 Seconds
(without alignments)
86.043 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360

Perfect score: 151

Sequence: 1 ERMALQTDIVDLQSPMGKQGGLDDLE 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	151	100.0	756	2	US-08-887-518-4
2	151	100.0	756	2	US-09-023-321-4
3	151	100.0	756	2	US-08-890-853-2
4	151	100.0	756	2	US-09-032-475-4
5	151	100.0	756	2	US-09-039-125A-2
6	151	100.0	756	2	US-09-099-124A-2
7	151	100.0	756	3	US-09-032-476-2
8	151	100.0	756	3	US-08-890-854-2
9	151	100.0	756	3	US-09-023-324-2
10	151	100.0	756	3	US-09-168-629-15
11	151	100.0	756	3	US-08-910-820-9
12	151	100.0	756	4	US-09-109-986-2
13	151	100.0	756	4	US-09-844-908-9
14	151	100.0	756	4	US-09-868-758-4
15	84	55.6	584	3	US-09-160-483-1
16	79	52.3	745	2	US-08-887-518-3
17	79	52.3	745	2	US-08-023-321-3
18	79	52.3	745	2	US-08-890-853-4
19	79	52.3	745	2	US-09-032-475-3
20	79	52.3	745	2	US-09-039-125A-4
21	79	52.3	745	2	US-09-099-124A-4
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23	79	52.3	745	3	US-08-890-854-4
24	79	52.3	745	3	US-09-023-324-4
25	79	52.3	745	3	US-09-168-629-2
26	79	52.3	745	3	US-08-910-820-10
27	79	52.3	745	3	US-08-810-131A-2

28	79	52.3	745	4	US-09-109-986-4	Sequence 4, Appli
29	79	52.3	745	4	US-09-844-908-10	Sequence 10, Appl
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31	76	50.3	996	4	US-09-417-197-123	Sequence 123, App
32	76	50.3	997	4	US-09-417-197-121	Sequence 121, App
33	55	36.4	406	4	US-09-252-991A-32895	Sequence 32895, A
34	54	35.8	388	4	US-08-178-257-15	Sequence 15, Appl
35	54	35.8	390	4	US-09-489-039A-8065	Sequence 8065, Ap
36	54	35.8	396	4	US-09-252-991A-18619	Sequence 18619, A
37	51	33.8	551	4	US-09-543-681A-7532	Sequence 7532, Ap
38	50	33.1	735	4	US-09-252-991A-32240	Sequence 32240, A
39	49	32.5	397	4	US-09-543-681A-5675	Sequence 5675, Ap
40	49	32.5	761	4	US-09-198-452A-335	Sequence 335, App
41	48.5	32.1	374	4	US-09-252-991A-23582	Sequence 23582, A
42	48	31.8	539	3	US-08-687-590-27	Sequence 27, Appl
43	48	31.8	539	4	US-09-702-705-326	Sequence 326, App
44	48	31.8	539	4	US-09-736-457-326	Sequence 326, App
45	48	31.8	539	4	US-09-614-124B-326	Sequence 326, App

ALIGNMENTS

RESULT 1

US-08-887-518-4
; Sequence 4, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-4

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 2, 4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ERMALQTDIVDLQSPMGKQGGLDDLE 30
Db 535 ERMALQTDIVDLQSPMGKQGGLDDLE 564

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RESULT 2
US-09-023-321-4
; Sequence 4, Application US/09023321
; Patent No. 584073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; APPLICANT/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-4

Query Match          100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred.No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ERMALQTDIVDLQSPMGRKGGTLDLLE 30
Db      535 ERMALQTDIVDLQSPMGRKGGTLDLLE 564

RESULT 3
US-08-890-853-2
; Sequence 2, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-2

Query Match          100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred.No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ERMALQTDIVDLQSPMGRKGGTLDLLE 30
Db      535 ERMALQTDIVDLQSPMGRKGGTLDLLE 564

RESULT 4
US-09-032-475-4
; Sequence 4, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-4
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Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
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 Db 535 ERMALQTDIVDLQSPMGRKQGGTLDLLE 564

RESULT 5

US-09-099-125A-2
 ; Sequence 2, Application US/09099125A
 ; Patent No. 5916760
 ; GENERAL INFORMATION:
 ; APPLICANT: Goeddel, David V.
 ; APPLICANT: Woronicz, John
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/099,125A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/890,853
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-006-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 756 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; APPLICATION TYPE: peptide
 ; US-09-099-125A-2

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
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 Db 535 ERMALQTDIVDLQSPMGRKQGGTLDLLE 564

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
 |||||
 Db 535 ERMALQTDIVDLQSPMGRKQGGTLDLLE 564

RESULT 6

US-09-099-124A-2
 ; Sequence 2, Application US/09099124A
 ; Patent No. 5939302
 ; GENERAL INFORMATION:
 ; APPLICANT: Goeddel, David V.
 ; APPLICANT: Woronicz, John
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,124A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,853
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 756 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-124A-2

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
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 Db 535 ERMALQTDIVDLQSPMGRKQGGTLDLLE 564

RESULT 7

US-09-032-476-2
 ; Sequence 2, Application US/09032476
 ; Patent No. 6235492
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothe, Mike
 ; APPLICANT: Cao, Zhaodan
 ; APPLICANT: R gnier, Catherine
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/032,476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/890,854
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:

Query Match 100.0%; Score 151; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
 |||||
 Db 535 ERMALQTDIVDLQSPMGRKQGGTLDLLE 564

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; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-476-2

Query Match 100.0%; Score 151; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDLE 30
DB 535 ERMALQTDIVDLQSPMGKKGGLDLE 564

RESULT 8
US-08-890-854-2
; Sequence 2, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-854-2

Query Match 100.0%; Score 151; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDLE 30
DB 535 ERMALQTDIVDLQSPMGKKGGLDLE 564

RESULT 9
US-09-023-324-2
; Sequence 2, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-324-2

Query Match 100.0%; Score 151; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDLE 30
DB 535 ERMALQTDIVDLQSPMGKKGGLDLE 564

RESULT 10
US-09-168-629-15
; Sequence 15, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: IKK Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-15

Query Match          100.0%; Score 151; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGLDLE 30
Db 535 ERMALQTDIVDLQSPMGRKQGGLDLE 564

RESULT 11
US-08-910-820-9
; Sequence 9, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-910-820-9

Query Match          100.0%; Score 151; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGLDLE 30
Db 535 ERMALQTDIVDLQSPMGRKQGGLDLE 564

RESULT 12
US-09-109-986-2
; Sequence 2, Application US/09109986
; Patent No. 6479266
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R grier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-109-986-2

Query Match          100.0%; Score 151; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMALQTDIVDLQSPMGRKQGGLDLE 30
Db 535 ERMALQTDIVDLQSPMGRKQGGLDLE 564

RESULT 13
US-09-844-908-9
; Sequence 9, Application US/09844908
; Patent No. 6576437
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,908
; FILING DATE: 27-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-908-9

Query Match 100.0%; Score 151; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
DB 535 ERMALQTDIVDLQSPMGKQGGTLDLLE 564
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RESULT 14
US-09-868-758-4
; Sequence 4, Application US/09868758
; Patent No. 6576439
; GENERAL INFORMATION:
; APPLICANT: Glaxo Wellcome KK
; APPLICANT: Takemoto, Yoshihiro
; APPLICANT: Sakai, Yutaka
; APPLICANT: Hashimoto, Yasuhiro
; TITLE OF INVENTION: IKK3
; FILE REFERENCE: 9950986P
; CURRENT APPLICATION NUMBER: US/09/868,758
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: GB 9828704.8
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-868-758-4

Query Match 100.0%; Score 151; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.4e-16; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
DB 535 ERMALQTDIVDLQSPMGKQGGTLDLLE 564
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RESULT 15
US-09-160-483-1
; Sequence 1, Application US/09160483A
; Patent No. 6083732
; GENERAL INFORMATION:
; APPLICANT: Marcu, Kenneth B.
; TITLE OF INVENTION: A BIOLOGICALLY ACTIVE ALTERNATIVE FORM OF THE IKK
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; TITLE OF INVENTION: ALPHA IKB KINASE
; FILE REFERENCE: Docket No. 6083732; 178-255
; CURRENT APPLICATION NUMBER: US/09/160,483A
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 584
; TYPE: PRT
; ORGANISM: mus.musculus domesticus
US-09-160-483-1

Query Match 55.6%; Score 84; DB 3; Length 584;
Best Local Similarity 46.7%; Pred. No. 1.8e-05;
Matches 14; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

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DB 532 DQIMSLHTEIMELQKSPYGRQGDLMESLE 561

Search completed: September 24, 2004, 09:46:43
Job time : 19 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 09:45:44 ; Search time 128 Seconds

(without alignments)
75.365 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360

Perfect score: 151

Sequence: 1 ERMWALQTDIVLQSPMGKQGGLDDLE 30

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Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	151	100.0	756	9	US-09-796-872-15
3	151	100.0	756	9	US-09-771-161A-232
4	151	100.0	756	9	US-09-844-908-9
5	151	100.0	756	9	US-09-844-988-9
6	151	100.0	756	14	US-10-243-408-2
7	151	100.0	756	14	US-10-338-462-9
8	151	100.0	756	15	US-10-408-636-4
9	151	100.0	756	12	US-10-394-322A-33
10	151	100.0	756	12	US-10-087-192-1758
11	79	52.3	745	9	US-09-796-872-2
12	79	52.3	745	9	US-09-844-908-10
13	79	52.3	745	9	US-09-844-988-10
14	79	52.3	745	12	US-10-060-065-14
15	79	52.3	745	14	US-10-243-408-4

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16 79 52.3 745 14 US-10-059-585-35 Sequence 35, Appl
17 79 52.3 745 14 US-10-338-462-10 Sequence 10, Appl
18 79 52.3 745 15 US-10-408-636-3 Sequence 3, Appl
19 79 52.3 745 15 US-10-394-322A-32 Sequence 32, Appl
20 79 52.3 745 16 US-10-741-601-375 Sequence 123, App
21 76 50.3 996 14 US-10-072-036-123 Sequence 123, App
22 76 50.3 997 14 US-10-072-036-121 Sequence 121, App
23 56 37.1 467 12 US-10-282-122A-67939 Sequence 67939, A
24 55 36.4 224 12 US-10-424-599-259148 Sequence 259148, A
25 55 36.4 482 12 US-10-424-599-199420 Sequence 199420, A
26 54 35.8 383 12 US-10-282-122A-69530 Sequence 69530, A
27 54 35.8 387 9 US-09-815-242-10416 Sequence 10416, A
28 54 35.8 387 9 US-09-815-242-13750 Sequence 13750, A
29 54 35.8 387 12 US-10-282-122A-56765 Sequence 56765, A
30 54 35.8 387 12 US-10-282-122A-60312 Sequence 60312, A
31 54 35.8 387 12 US-10-282-122A-73063 Sequence 73063, A
32 54 35.8 387 12 US-10-282-122A-75775 Sequence 75775, A
33 54 35.8 387 15 US-10-369-493-23631 Sequence 23631, A
34 54 35.8 388 16 US-10-357-521-15 Sequence 15, Appl
35 54 35.8 391 9 US-09-815-242-5123 Sequence 5123, Ap
36 54 35.8 391 12 US-10-282-122A-43443 Sequence 43443, A
37 54 35.8 391 12 US-10-282-122A-67603 Sequence 67603, A
38 54 35.8 391 15 US-10-447-515-26 Sequence 26, Appl
39 54 35.8 409 15 US-10-369-493-13890 Sequence 13890, A
40 53 35.1 387 12 US-10-282-122A-77565 Sequence 77565, A
41 53 35.1 507 15 US-10-369-493-10701 Sequence 10701, A
42 52 34.4 386 12 US-10-282-122A-56042 Sequence 56042, A
43 52 34.4 387 12 US-10-282-122A-77831 Sequence 77831, A
44 52 34.4 850 15 US-10-369-493-10111 Sequence 10111, A
45 51 33.8 331 16 US-10-437-963-173921 Sequence 173921,

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ALIGNMENTS

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RESULT 1
US-10-087-192-1755
; Sequence 1755, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric K.
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1755
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1755

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Query Match 100.0%; Score 151; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMWALQTDIVLQSPMGKQGGLDDLE 30
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Db 549 ERMWALQTDIVLQSPMGKQGGLDDLE 578

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RESULT 2
US-09-796-872-15
; Sequence 15, Application US/09796872
; Patent No. US20020045235A1
; GENERAL INFORMATION:

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; APPLICANT: Karin, Michael
; APPLICANT: DiDonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/796,872
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/168,629
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,470
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-872-15

Query Match 100.0%; Score 151; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDLE 30
Db 535 ERMALQTDIVDLQSPMGKKGGLDLE 564

RESULT 3

US-09-771-161A-232
; Sequence 232, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:

; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 232
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-232

Query Match 100.0%; Score 151; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDLE 30
Db 535 ERMALQTDIVDLQSPMGKKGGLDLE 564

RESULT 4

US-09-844-908-9
; Sequence 9, Application US/09844908
; Patent No. US20020151021A1
; GENERAL INFORMATION:

; APPLICANT: Mercurio, Frank
; Applicant: Zhu, Hengyi
; Barbossa, Miguel
; Li, Gian
; Murray, Brion W.

; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/844,908
; APPLICATION NUMBER: US/09/844,908
; FILING DATE: 27-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 756 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-908-9

Query Match 100.0%; Score 151; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKKGGLDLE 30
Db 535 ERMALQTDIVDLQSPMGKKGGLDLE 564

RESULT 5

US-09-844-988-9
; Sequence 9, Application US/09844988
; Patent No. US20020158764A1
; GENERAL INFORMATION:

; APPLICANT: Mercurio, Frank
; Applicant: Zhu, Hengyi
; Barbossa, Miguel
; Li, Gian
; Murray, Brion W.

; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


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; APPLICATION NUMBER: US/09/844,988
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,820
; FILING DATE: 1997-08-13
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-988-9

Query Match          100.0%; Score 151; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSRPMGRKQGGLDDLE 30
Db 535 ERMALQTDIVDLQSRPMGRKQGGLDDLE 564

RESULT 6
US-10-243-408-2
; Sequence 2, Application US/10243408
; Publication No. US20030077683A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; Cao, Zhaodan
; R. gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/243,408
; FILING DATE: 13-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/890,854
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-243-408-2

Query Match          100.0%; Score 151; DB 14; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSRPMGRKQGGLDDLE 30
Db 535 ERMALQTDIVDLQSRPMGRKQGGLDDLE 564

RESULT 7
US-10-338-462-9
; Sequence 9, Application US/10338462
; Publication No. US20030100026A1
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; Zhu, Hengyi
; Barbosa, Miguel
; Li, Gian
; Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/338,462
; FILING DATE: 08-Jan-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,908
; FILING DATE: 27-Apr-2001
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-338-462-9

Query Match          100.0%; Score 151; DB 14; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSRPMGRKQGGLDDLE 30
Db 535 ERMALQTDIVDLQSRPMGRKQGGLDDLE 564
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RESULT 8
US-10-408-636-4
; Sequence 4, Application US/10408636
; Publication No. US20030215879A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Wellcome KK
; APPLICANT: Takemoto, Yoshihiro
; APPLICANT: Sakai, Yutaka
; APPLICANT: Hashimoto, Yasuhiro
; TITLE OF INVENTION: IKK3 Kinase
; FILE REFERENCE: PJ3630US2
; CURRENT APPLICATION NUMBER: US/10/408,636
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB 9828704.8
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-636-4

Query Match      100.0%; Score 151; DB 15; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
Db 535 ERMALQTDIVDLQSPMGKQGGTLDLLE 564

RESULT 9
US-10-394-322A-33
; Sequence 33, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-33

Query Match      100.0%; Score 151; DB 15; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
Db 535 ERMALQTDIVDLQSPMGKQGGTLDLLE 564

RESULT 10
US-10-087-192-1758
; Sequence 1758, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122

Query Match      100.0%; Score 151; DB 15; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
Db 535 ERMALQTDIVDLQSPMGKQGGTLDLLE 564

RESULT 11
US-09-796-872-2
; Sequence 2, Application US/09796872
; Patent No. US20020045235A1
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: DiDonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: IxB Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/796,872
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/168,629
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,470
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-872-2

Query Match      52.3%; Score 79; DB 9; Length 745;
Best Local Similarity 43.3%; Pred. No. 0.0023;
Matches 13; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
Db 532 DQIMSLHAEIMELQSPYGRQGLMESLE 561

RESULT 12
US-09-844-908-10
; Sequence 10, Application US/09844908
; Patent No. US20020151021A1
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brian W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP

Query Match      52.3%; Score 79; DB 9; Length 745;
Best Local Similarity 43.3%; Pred. No. 0.0023;
Matches 13; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGKQGGTLDLLE 30
Db 532 DQIMSLHAEIMELQSPYGRQGLMESLE 561
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Matches 13; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
DB 532 DQIMSLHAEIMELQSPYGRROGDLMESLE 561

RESULT 15

US-10-243-408-4
; Sequence 4, Application US/10243408
; Publication NO. US2003007683A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; Cao, Zhaodan
; R Guier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/243,408
; FILING DATE: 13-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/890,854
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-243-408-4

Query Match 52.3%; Score 79; DB 14; Length 745;
Best Local Similarity 43.3%; Pred. No. 0.0023;
Matches 13; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 ERMALQTDIVDLQSPMGRKQGGTLDLLE 30
DB 532 DQIMSLHAEIMELQSPYGRROGDLMESLE 561

Search completed: September 24, 2004, 09:57:09
Job time : 128 secs